

TABLE 1

Bacteriophage 44AHJD, complete genome sequence.

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1      tccattttctt tactaaactt aaaaatgctg tgcaacaact taaccaactt atctaacctt
61     ttacatatctc atcaaatata aaatttatgt atctattgac ttttattcaa aattatgatt
121    tcaacatata ataaaaattaa tttacttatt taaatattct atgatataat tagttataaa
181    atatttggag gtgtataaat gacagaatgt gatgaaatcg taaaaccaga cgacaaagaa
241    gaaacttcag aatcaactga agaaaattta gaatcaactg aagaaacttc agaatcaact
301    gaagaatcaa ctgaagaatc aactgaagaa tcaactgaag ataaaacagt agaaacaatc
361    gaagaagaaa atgaaaacaa attagaacct actacaacag atgaagatag ttcgaaatgt
421    gaccctgttg tattagaaca acgtattgct tcattagaac aacaagtgcg tactttttta
481    tcttcacaaa tgcaacaacc acaacaagta caacaaacac aatcagatgt aacagaatca
541    aacaaagaag ataacgacta ttcagatgaa gaactagttg ataagttaga tttagattag
601    gaggaatttta aacatgtatg agggaaacaa catgcgttct atgatgggta catcatatga
661    agattcaaga ttaaataaac gaacagaatt aaatgaaaac atgtcaattg atacaaataa
721    aagtgaagat agttatggtg tacaaattca ttcactttca aaacaatcat ttacaggtga
781    cgttgaggag gaataataaa ttatggcaca acaatctaca aaaaatgaaa ctgcactttt
841    agtagcaaag tcagctaaat cagcgttaca agattttaat catgattatt caaaatcttg
901    gacatttggc gacaaatggg ataattcaaa tacaatgttc gaaacatttg taaataaata
961    tttattccct aagattaatg agactttatt aatcgatatt gcattaggta atcgttttta
1021   ttggtttagct aaagagcaag attttatttg acaatatagt gaagaatacg tgattatgga
1081   cacagtacca attaacatgg acttatctaa aaatgaggaa ttaatgttga aacgtaatta
1141   tccacgtatg gcaactaagt tatatggtaa cggaattgtg aagaaacaaa aattcacatt
1201   aaacaacaat gatacacgtt tcaatttcca aacattagca gacgcaacta attacgcttt
1261   aggtgtatag aaaaagaaaa tttctgatag taatgtatta gaagaaaaag aaatgcgtgc
1321   aatgtttagt gattactcat tgaatcaatt atccgaaaca aatgtacgta aagcaacatc
1381   aaaagaagat ttagcaagca aagtttttga agcaatccta aacttacaaa acaacagtgc
1441   taaatataat gaagtacatc gtgcatcagg tgggtgcaatt ggacaatata caactgtatc
1501   aaaattaaaa gatattgtga ttttaacaac agattcatta aaatcttacc ttttagatac
1561   taagattgca aacacattcc agattgcagg cattgatttc acagatcacg ttattagttt
1621   tgacgactta ggtggcgtgt ttaaagtaac aaaagaattt aagttacaaa accaagattc
1681   aattgacttt ttacgtgctg atggagatta tcaatcaca ttaggagata caattccagt
1741   tgggtgctgta tttacttatg atgtatctaa acttaaagag tttactggca acgttgaaga
1801   aattaaacca aaatcagatt tatatgcgtt tattttggat attaatcaa ttaaataata
1861   acgttacaca aaaggtatgt taaaaccacc attccataac cctgaatttg atgaagttac
1921   aactgggatt cattactatt catttaaagc cattagtcca ttctttaata aaattttaat
1981   tactgaccaa gatgtaaatt caaaaccaga ggaagaatta caagaataaa aggagcgtaa
2041   aatatgaaca acgataaaa aggtttaaac gttgagttat caaaggaaat cagcaaaaga
2101   gttgttgaac atcgcaacag atttaaactg cttatgttta atcgttattt ggaattttta
2161   ccgctactaa tcaactatac caatcgtgat acggttggtg tagattttat tcagttagaa
2221   tcagctttta gacaaaacat taatgtagtt gttggtgaag ctagaataaa gcaattatg
2281   attccttggt atgtaaataa cacttacttt aatcaagcac caaatttttc atcaaacttt
2341   aatttccaat ttcaaaaacg attaactaaa gaagatatat attttattgt acctgactat
2401   ttaataacct atgattgtct acaaattcat aagctatatg ataactgtat gagtggtaac
2461   tttgttgtca tgcaaaataa accaattcaa tataatagt atatagaat tatagaacat
2521   tatactgatg aattagcaga agttgcttta tctcgctttt cttaaatcat gcaagcaaaa
2581   tttagcaaga tatttaaact agaaattaat gacgagtcaa tcaatcaact tgtgtccgaa
2641   atatataacg gtgcaccatt tgttaaaatg tcacctatgt ttaatgcaga tgacgatatc
2701   attgatttta caagtaatat cgtaatccca gcattaactg aaatgaaacg ggaatatcaa
2761   aacaaaatta gtgaattaag taactattta ggcattaatt cattagccgt tgataaagaa
2821   agcgggtgtt cagacgaaga ggcaaaaagt aatcgtggat ttaccacatc aaacagtaat
2881   atctatttta aaggtcgtga accaattacg tttttatcaa agcgttatgg tttagatatt
2941   aaaccgtatt acgatgatga aacaacgtct aaaatatcaa tggtagacac actttttaaa
3001   gatgaaagca gtgatataaa tggctagata cacaatgact ttatacgatt tcattaaatc

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TABLE 1

3061	agaattgatt	aaaaaagggtt	tcaatgaatt	tgtaaattgat	aataaattaa	cgttttatga
3121	tgatgaattt	caattcatgc	aaaaaatgct	gaagttcgac	aaagacgttt	tagctatcgt
3181	taatgaaaaa	gtattttaaag	gtttttcatt	gaaagatgaa	ttatcagatt	tacttttttaa
3241	aaaatcattt	acgattcatt	ttttagatag	agaaatcaac	agacaaacag	ttgaagcatt
3301	tggcatgcaa	gtgattactg	tatgtattac	acatgaggat	tattttaaag	tggttttattc
3361	atcaagtcaa	gttgaaaaat	acttacaatc	acaaggcttc	acagaacaca	atgaagatac
3421	aacaagtaac	actgatgaaa	catcgaatca	aaatgctaca	tcttttagaca	attcaactgg
3481	catgactgca	aacagaaaacg	cttatgtgtc	attaccacaa	agtgagggtta	acattgatgt
3541	tgataataca	acgtttacgat	tcgctgataa	taatacagatt	gataacggta	aaactgtgaa
3601	taaatcgagt	aacgaaagta	atcaaaacgc	aaaacgtaat	caaaatcaaa	aaggtaatgc
3661	aaaagggtaca	caattcacta	agcagtattt	aattgataat	attgataaag	cgtacgattt
3721	aagaaaagaaa	atttttaaag	aatttgataa	aaaatgtttt	ttacaaattt	ggtagagggtg
3781	gttaaataat	ggcatataat	gaaaacgatt	ttaaatat	tgatgacatt	cgtccatttt
3841	tagacgaaat	ttataaaaacg	agagaacggt	atacaccggt	ttacgatgat	agagcagatt
3901	ataatactaa	ttcaaaatca	tattatgatt	atattttcaag	attatcaaaa	ctaattgaag
3961	tattagcacg	tcgtatttgg	gactatgaca	atgaattaaa	aaaacgtttc	aaaaattggg
4021	acgacttaat	gaaagcattt	ccagagcaag	cgaaagactt	atttagagggt	tgggttaaagc
4081	acggtacgat	tgacagtatt	attcatgacg	agtttaaaaa	atatacgca	ggattaacat
4141	cggcatttgc	tttattttaa	gttactgaaa	tgaacaaaat	gaatgacttt	aaatcagaag
4201	ttaaagactt	aattaaagat	attgaccgtt	tcgttaattg	gtttgaatta	aatgagcttg
4261	aaccaaagtt	tgtgatgggc	tttgggtggt	ttcgcaacgc	agtttaacca	tctattaata
4321	ttgataaaga	aacaaatcac	atgtactcta	cacaatccga	ttctcaaaaa	cctgaagggtt
4381	tttgataaaa	taaattaaca	cctagtgggtg	acttaatttc	aagcatgcgt	attgtacagg
4441	gtggtcatgg	tacaacaatc	ggattagaac	gtcaatccaa	tgggtgaaatg	aaaatctggt
4501	tacatcacga	tgggtgttgc	aaactgttac	aagtcgcata	taaagataat	tatgtattag
4561	atttagaaga	ggctaaaggt	ttaacagatt	atacaccaca	gtcactttta	aacaaacaca
4621	catttacacc	gttaattgat	gaagcaaag	acaaactcat	tttaagattc	gggtacggaa
4681	caatacaggt	tcgttcaaga	gcagacgtaa	aaaatcacat	tgataatgta	gaaaaagaaa
4741	tgacaattga	taattcagaa	aacaatgata	atcgttggat	gcaaggcatt	gctgttgatg
4801	gtgatgattt	atactgggtt	agtggtaaca	gttcagttta	ttcacatgtt	caaactcggt
4861	aatattcatt	aacaacaggt	caaaagattt	atgattatcc	atttaagtta	tcatatcaag
4921	acggtattaa	tttcccacgt	gataacttta	aagagcctga	gggtatttgc	atttatacaa
4981	atccaaaaac	aaaacgtaaa	tcgttattac	ttgctatgac	aaacggcggg	gggtggaaaac
5041	gtttccataa	tttatatggt	ttcttccaac	ttgggtgagta	tgaacacttt	gaagcattac
5101	gcgcaagagg	ttcacaaaac	tataaattaa	caaaagacga	cggctcgtgca	ttatctattc
5161	cagaccatat	cgacgattta	aatgacttaa	cgcaagctgg	tttttattat	attgacgggg
5221	gtactgcaga	aaaacttaag	aatatgccaa	tgaatggtag	caagcgtata	attgacgctg
5281	gttggttcat	taatgtatac	cctacaacac	aaacattagg	tacggttcaa	gaattaacac
5341	gtttctcaac	aggtcgtaaa	atgggttaaaa	tgggtgcgtgg	tatgacttta	gacgtattta
5401	cgttaaaaatg	ggattatgga	ttatggacaa	caatcaaaaac	tgacgcacca	tatcaagaat
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5521	acattacagg	taaccaaatg	gaattattta	gagacgcgcc	agaagaaatt	aaaaaagtgg
5581	gtgcatgggt	acgtgtgtca	agtggtaacg	cagtcggtga	agtaagacaa	acattagagg
5641	ctaatatatc	ggaatataaa	gaattcttca	gtaatgttaa	tgcggaacaa	aaacatcgtg
5701	aatatggttg	ggtagcaaaa	catcaaaaat	aggagtgata	taaatgaaat	cacaacaaca
5761	agcaaaagaa	tggatatata	agcatgaggg	ggcagggtgtt	gactttgatg	gtgcatatgg
5821	atttcaatgt	atggacttat	cagttgctta	tgtgtattac	attactgacg	gtaaagttcg
5881	catgtggggg	aatgctaaag	acgcgataaa	taatgacttt	aaagggttag	cgacgggtgta
5941	taaaaaataca	ccgagcttta	aacctcaatt	aggggacggt	gctgtatata	caaattggaca
6001	atatggacat	attcaatgtg	tgtaaagtgg	aaatcttgat	tattatacat	gcttagaaca
6061	aaactgggtta	ggcggcggtt	ttgacgggtt	ggaaaaagca	accattagaa	cacattatta
6121	tgacgggtgta	actcacttta	ttagacctaa	attttcaggt	agtaatagca	aagcattaga
6181	aacatcaaaa	gtaaatacat	ttggaaaatg	gaaacgaaac	caatacggca	catattatag

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6241	aaatgaaaat	ggtacattta	catgtgggtt	tttaccaata	tttgcacgtg	tcggtagtc
6301	aaaattatca	gaacctaatg	gctattgggt	ccaaccaa	ggttatacac	catataacga
6361	agtttggtta	tcagatgggt	acgtatggat	tggttataac	tggaaggca	cacgttatta
6421	tttaccagtg	cgccaatgga	atggaaaaac	aggtaatagt	tacagtgttg	gtattccttg
6481	gggggtgttc	tcataatggg	tatttttagcc	tttttctttg	aatttagttg	gaaaagatac
6541	aaataagagg	tgtaaacaat	ggctgataga	atcgtaagaa	gtttaagaca	agttgaaaca
6601	attgaacgtt	tattggagga	aaaaaatgag	aaagttaacg	aattttaagt	ttttctataa
6661	cacaccgttt	acagactatc	aaaacacgat	tcattttta	agtaataaag	aacgtgatga
6721	ttattttttta	aatggtcgtc	attttaaatc	gtagactat	tcaaaacaac	cgtataat
6781	tatactgat	agaatggaaa	tcaatgttga	tatgcagtgg	catgacgcac	aaggatttaa
6841	ctacatgacg	tttttatcag	attttgagga	tagaagatat	tacgtttttg	taaaccaaat
6901	cgaatacgtg	aatgacgttg	tggttaaaat	atattttgtc	attgatacca	ttatgacgta
6961	tacacaaggg	aatgtattag	agcaactctc	aaacgtcaat	attgaacgtc	aacattttatc
7021	aaaacgcacg	tataactata	tgttaccaat	gttacgtaat	aatgatgatg	tgtaaaagt
7081	atcaataaaa	aactatgttt	ataaccaa	gcaacaatat	ttggaaaatt	tagtattatt
7141	ccagtcaagc	gctgatttat	caaagaaatt	tggtactaaa	aaagagccaa	acttagatac
7201	gtcaaaaggt	acgatttatg	acaatatcac	atcaccagtc	aacttatacg	ttatggaata
7261	tggtgacttt	attaacttta	tggtataaa	gagtgcctat	ccatggatta	cgcaaaactt
7321	tcaaaaggtt	caaagtgtac	ctaaagactt	tattaatata	aaagacttag	aggacgttaa
7381	aaccagtga	aaaattacag	gattaaaaac	attaaaacag	ggtggtaaat	caaaagaatg
7441	gagtctaaaa	gatttatcat	taagtttctc	aaatcttcaa	gagatgatgt	tatctaaaaa
7501	agatgaat	aaacatatga	tacgtaatga	gtatatgaca	attgaat	atgactggaa
7561	tggaataacg	atgttactcg	acgctggtaa	gatttcacaa	aaaactgggtg	ttaagttacg
7621	tacaaaatca	attattgggt	atcataatga	agttcgagta	tatccagtag	attataacag
7681	tgctgaaaac	gacagaccaa	tactcgctaa	aaataaagaa	atattgattg	atacgggttc
7741	attcttaaat	acaaatataa	catttaatag	ttttgcacaa	gtaccaatat	taatcaataa
7801	tggtatctta	ggacaatcac	aacaagccaa	ccgacaaaaa	aatgcagaaa	gtcaattaat
7861	tacaaatcgt	attgataatg	tattaaatgg	tagcgacccg	aatcacgct	tttatgacgc
7921	tgtgagtgt	gcaagtaatt	taagtccaac	tgctttat	ggtaagt	atgaagaata
7981	taatttctac	aaacaacaac	aagctgaata	taaagatt	gccttacaac	caccttctgt
8041	aactgaatca	gaaatgggca	acgcattcca	aattgcgaat	agcattaacg	gtttaacgat
8101	gaaaattagt	gtaccgtcac	ctaaagaaat	tacattttta	caaaaatatt	atatgttgtt
8161	tggttttgaa	gtgaatgact	ataattcatt	tattgaacca	attaacagta	tgactgtttg
8221	caattattta	aaatgtacag	gtacgtatac	tatacgtgac	atcgaccca	tgtaaatgga
8281	acaattaaaa	gcaatttttag	aatctgggtg	aagattttgg	cataatgacg	gttcaggtaa
8341	tccaatgtta	caaaatccat	taaataacaa	atthagagag	gggtataat	atgaacgaag
8401	taaaattcag	atttacagac	tcagaagcgt	ttcacatgtt	tatatacgtc	ggggatttaa
8461	aattactcta	ctttttat	gtattaatgt	tcgttgatat	tattacaggt	atttcaaaag
8521	caattaaaaa	taataactta	tggtcaaaaa	aatcaatgag	aggattttct	aaaaaattat
8581	tgatattctg	tattatcatt	ttagcaaaca	tcattgacca	gattttacaa	ttaaaagggtg
8641	gtctactcat	gattacaata	ttttattata	ttgcaaata	gggactttct	attgtagaaa
8701	attgtgcaga	aatggacgta	ttagtaccag	aacaaattaa	agataaatta	agagtcatta
8761	aaaatgatac	tgaaaagagt	gataacaatg	aacgatcaag	agaagataga	taaatttacg
8821	cattcctata	ttaatgatga	ttttggttta	acgatagacc	agttagtccc	taaagtaaaa
8881	ggatatgggc	gctttaatgt	atggcttggt	ggtaatgaaa	gtaaaatcag	acaagtatta
8941	aaagcagtaa	aagagatagg	tgtttcacct	actctttttg	ccgtatatga	aaaaaatgag
9001	ggttttagtt	ctggacttgg	ttggttaaac	catacgtctg	cacgtggtga	ttatttaaca
9061	gatgctaaat	tcatagcaag	aaagttagta	tcacaatcaa	aacaagctgg	acaaccgtct
9121	tggtatgacg	caggtaacat	cgtccacttt	gtaccacaag	acgtacaaag	aaaaggtaat
9181	gcagattttg	caaaaaatat	gaaagcaggt	acaattggac	gtgcatatat	tccattaaca
9241	gcagctgcta	cttgggcggc	atattatcct	ttaggtttga	aagcatcata	taacaaagta
9301	caaaactatg	gtaatccatt	tttagacggt	gcgaatacta	ttctagcttg	gggtggtaaa
9361	ttagacggta	aagggtggatc	acctagtgat	tcgtctgaca	gtggtagtag	tggtgacagt

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9421	ggtagttcac	tactcgcttt	agcaaaacaa	gccatgcaag	aattattaaa	aaaaatacaa
9481	gacgcattac	aatgggacgt	tcatagtatt	ggtagtgata	aatttttttag	taatgattat
9541	tttacattag	aaaaaacatt	taacaacaca	tatcatatta	aaatgacgat	tggtttactt
9601	gattcattaa	aaaaactgat	tgatagcggt	caagtagata	gtgggagtag	tagtttcta
9661	cctactgatg	atgacggaga	ccataaacca	attagtggta	aatcagtcaa	gccaaatgga
9721	aaaagtggtc	gtgtgattgg	tggtaactgg	acatatgcac	agttaccaga	aaaatataaa
9781	aaagcaattg	gtgtaccttt	attcaaaaaa	gaatacttat	acaaaccagg	taacatattt
9841	cctcaaacgg	gtaatgcagg	acaatgtaca	gaattaacat	gggcgtatat	gtcacaacta
9901	catggtaaaa	gacaacctac	cgacgcagg	caaataacaa	acggtcagcg	tgtatggtac
9961	gtctataaaa	agttaggtgc	aaaaacaaca	cataatccaa	cagtaggtta	tggtttctct
10021	agtaaaccac	catacttaca	agcaactgca	tatgggtattg	gtcacacagg	tgttggtgta
10081	gcagtttttg	aagatgggtc	gttttttagtt	gcaaaactata	atgtaccacc	atatgttgca
10141	ccatcacgtg	tggtattgta	tacactcatt	aatggcgtag	caaataatgc	tgggtgataat
10201	attgtattct	ttagtgggtat	tgtttaatta	actatgctat	aatgaacaca	tgctagtaat
10261	gctagtaaat	aaaatacaaa	acataatcaa	ttttcgtaca	cattttttcat	gttatctcaa
10321	aaagaaaagg	agactgttat	tttaacagtt	gccttttttt	atttcatcat	gttcacgttt
10381	taatatatgc	aaatcagatt	tgttatgtac	tgaacgttca	actggaaata	agtcgttaag
10441	tgaaaatgaa	ccgatgtcac	tttcaatata	agaatatca	tcaaattgac	tatgggtcgaa
10501	attttctcta	gcgtctttta	atataaaattc	acgttttcata	ttaagttcat	cagtaaaata
10561	ttcatcatat	acattaccac	atacaatttc	agtttttagac	ggatataatcg	atattgtacc
10621	ttgctcatta	tagatacttt	tattgttttc	aataatggca	ccgtcaaaga	attgttcacg
10681	tacaaagggt	tcaaaatcga	cgcttgatc	aaaggcggtt	ttcggtatac	cagcagaagc
10741	aattttaatc	tttccattca	cttcatatgc	atatttctta	tgattcagta	caaacatctt
10801	atctatctgt	tcgttttcaa	tatcccattt	acctaaggct	atcggtcgca	ataaactggg
10861	gttcaataag	ggtttaacaa	cggatttcat	atacaaaacta	tcagtatcgc	aataaataaa
10921	attgtcgtca	atttcacttt	ccgttaagta	ttggaaagga	accaataagt	tatacaatga
10981	acgtgatgtg	acaaatgtag	agaataatat	attacgttca	gtgtttttgt	aaccgttaat
11041	gatattgtat	agttcattgt	tatcatctaa	acggaataag	ttaaaatgtg	aacgtaatgc
11101	aggtatgcc	tataatccat	ttaaaacgac	tttagataac	ataacctcct	catttgagta
11161	tgggtgttcg	ttgatatcat	cagtaatgtg	atagtcgtaa	gggtgatgtca	tattgatttt
11221	gttttttaac	ttacottgtg	ttttaataaa	atagttttga	aaaataatat	cacgtgcatg
11281	aaagtattca	cattcatata	taacaaacga	attaacacgt	atatgcatgc	aatcaatacc
11341	cgtaatgtct	tgaatcattc	ttaatgtatt	tgtattgata	ttaacgtaat	cattatcatt
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11461	atcgttaaat	acatctttat	caatcttata	taatgaaaaa	taattgtcat	catctaaaaa
11521	agtagggatt	aacgttgggt	ctgaatagtg	ttcgtaaaaag	tataaccatg	ttggaatttt
11581	ttcatgatac	atcacataag	gataactcga	attgatgtca	atagaaaaac	aaggctcatc
11641	aattagtttg	tttatgtatt	tgggtgttata	catattttaa	ccaccacgat	agaatgattt
11701	aatatagtc	taaaaattca	tatcatggaa	atgataatgt	gtataagata	ttttaatatc
11761	ttgatattgg	ttgagtaact	gaaaacgtgt	catttcatta	ttcaagtaag	attccataat
11821	attcaatgaa	aatgttaatt	tgttatagtc	aaaatttgga	aatatatcac	tataatgaat
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12061	aagtaatttc	ttacctaatg	ttgcaattga	tgtattgggt	ttcataaagt	tatcaataat
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12361	gataatatct	gtttttgatt	ttgtgattgt	atcacgtctt	ttcacatacg	tataaaatgc
12421	gtcataaaaa	gattcgaaac	tcggaaatac	ttcaacatca	atttcataac	cattaaacca
12481	accaattgct	acagaataag	taacgttttt	atatttggtt	ggtttttttc	gtccgttaac
12541	tttattgtac	gctaattgtt	ctatatccca	gtataaaatc	attcgacgtt	catgtttatg

TABLE 1

12601	atattgcatg	cattctagta	atcccataat	cttacacacc	ttttataagc	catattgttt
12661	cattagatac	tttttcgtat	tctctatata	gttatcttcg	tatatTTTTT	cttttctttc
12721	aaactcactc	atatttttct	tcattttcatt	ttttatatga	aattttataa	ttttattcat
12781	atctaaatat	aaatatctat	cattatcaac	cacgtaattt	ttagagtaag	cattgtcaaa
12841	atgtaaattg	cttggattgt	agtaataacg	ttccatgttt	tctttataaa	acatatcatc
12901	acgtaaatag	gtaacatgat	tgtctatata	cctaatttta	gtacaaaatt	catattgttt
12961	tgtatatggg	acaacgataa	tatttgtcat	aaaagtagtt	acattataca	tgactttaat
13021	atattttatca	tcagttttga	tatagaagaa	atcaccgttt	tgattgatgt	gatttcttaa
13081	attatcatcc	gccaaattat	attcgttaaa	ttcaaattct	ccagttgtca	tagcgtcgtc
13141	atttgaatta	aacgcacgtg	tgttacgttt	ttcattcacg	taatcgtttc	gtcgcatttc
13201	taaaaaaatg	tttttgtaaa	gtcttgatgt	attcatttta	tgcttttgta	ataaattgta
13261	tatatTTTaa	ttggataata	taggacttga	aaagttgact	gcattaccta	gtaaaaacat
13321	tttagggaat	ccaatataat	caacgttacc	atgggttacg	tcgattgatt	catatatgtt
13381	ttttaactta	tcccactcat	caattaaata	atcatcttca	agtgctaaaa	actcatcata
13441	tataataata	ggatagtgtt	ttaaaaagtt	agaatgatat	tttaaattcag	tggcactatt
13501	caaactctgta	atcacaccaa	tttctttatc	ttgatagata	atagctaaat	agtccttagc
13561	acttctgaac	gtgacacgtt	ttgatTTTaa	tagtggattt	tcactctatga	tttcttcaat
13621	aaaatcacgg	taagcgtcac	gtaatgtata	atgacgtgat	aataaagtaa	atTTTtatc
13681	aagtTTaata	gctaaataaa	taaaaaatga	aacatagttg	aacgattttc	catcagaacg
13741	gtttgaaata	gatataataa	aatctatata	atcattcata	agttcatcaa	ctaattctat
13801	ttgattatac	ttatctggga	ttttttttct	gacatgattg	acagcatttt	gataatctct
13861	taccatgtct	aaacgatttt	gttttaccat	gtttttgctc	cttgtaatag	tttatgatgt
13921	cgtttacagt	gttaaattta	ttcgtcaaat	gttgcataat	ataaaaaagt	atacctcaca
13981	tcttcatcat	caatatTTgt	cactgggtct	tctgattttac	caatttcttt	atataaagta
14041	tcgatttctt	taatatattt	atacattgaa	gaattattat	ttttagcttg	taaattatat
14101	aaagcgtatt	tatgcttttt	agcgttttta	ttattagaat	catcattacg	gttatatatt
14161	tcaagaatat	aattttaatt	tttatgtctt	gaacctctta	ccaatgatac	agcatttaca
14221	tatgatacgt	ttctttcttt	aggaaaatag	ggcagatgtg	caaaatgttt	ccatgtgtca
14281	atgtacgcct	cttgtaaaatc	tttatcatca	aattttaaaat	taacattact	aaaatcattt
14341	aaaaataaat	ctttttcttg	ctcttttcta	gcttctcttt	cttttttcca	tctatccatt
14401	tcagacgtat	gtctaaccac	tgttatcaac	ctccatataa	agcataaata	accattaaaa
14461	agataatata	gaatataatc	aatgtagtga	ataaaacacc	aaatgacacg	cgtatatgca
14521	gtgtcataag	tatgataagt	gtaattaaaa	atgctaaaag	gaaaacaatg	gctatgttta
14581	ataggttatt	catgggtcaat	cactttccca	ttatcgtata	tgactttgtt	ttgataaata
14641	atcattaatt	cgctttcaag	agggttatca	aaatttgata	atacgtcgtc	aattgtaacg
14701	tttaataaaaa	tttctcttat	taattcatta	cttaaataat	ttctataata	aaatacaagt
14761	atattaaaaa	catgtttttt	aatatcaatg	tcgatatcta	acgtaaataa	ctctttttca
14821	atTTcaaaat	catcatattg	tttgtcaaac	tcaatataca	catcacccat	atTTattttt
14881	actatacatt	ttttattaga	tgaagtaaat	ttttcaaatt	tatcattata	ataatctcta
14941	tttgTTaaaa	ggtaataaat	taaattattt	aatctaaaag	tagttttta	tttcattttt
15001	atatctcctt	aatgtattct	atgatatacg	cgtatttttt	agtgaacagg	ttatattcat
15061	aatatgaata	tacaacttta	gcgtcatata	aatcttcaaa	cattgagatt	tgatgtggaa
15121	aatgtccttt	aatctcatcg	caatataata	ataccgtttt	gtattttacg	tccatttaaa
15181	cacctcataa	aaaatagggg	ataagtatcc	cctatgaaat	tgtattaaaa	tgatacttga
15241	ccaaaattga	ttgagtaacc	tttttgacct	tttttgTTTT	catattcata	aattgtgaat
15301	tgaacttctc	cagcattgat	aatgtcaaca	acgtcctcat	ctgctctcat	ttctttaatt
15361	aattctgtta	agtggttcgg	taagtttacg	ttatagtcac	cagtgcacgat	aacaccttgt
15421	tcaccgaatt	ttgattcttt	gtttgtgaat	aatgctctaa	cgatatactc	ttttttcata
15481	ccgtattttt	ctactaattc	tgatagtttg	ataaattctc	tttctttttc	ctcaaattca
15541	aatctcgcta	atgtgttttg	gtgtcttgat	aaaatatctt	ttacgtttgt	catttttatt
15601	ctcctcttat	ttaaattatt	tgctttctgc	aattgctgatt	tgtagtaaat	cattgtaata
15661	aacttgaatt	gttttcgttg	tgctgtgagt	ggacaatagt	ttacatgtgt	ctggtaataa
15721	ttcttttgct	tgtgttttg	ttaaatgata	ctcgtgaagt	ggtaaaaaat	cctcaatgta

TABLE 1

15781	ttcattatca	tcatctaagt	aatgaagtat	ataacctttg	acacgtaagg	taacaatgtc
15841	gtcaactttc	attattatat	cactcctttc	taaaaaacgt	aaacgttata	cgtttcataa
15901	aatcctttat	gcataattcca	ttgttctatt	gggtcatcac	cagcaatata	agacaatatt
15961	gattctgggt	tagtttcgtt	gtttagttca	tcatttaaga	attgaacaac	agaactatta
16021	tagtttaata	atagttgttg	gcaagccgat	aataagttaa	ttgcattgtc	aaatgtataa
16081	gctggattcc	attgaatcag	tttattgaat	agttgcaaca	tttcagtata	ggcttgtcct
16141	ttttcttctg	gtgcattatc	aacattaacc	attattatca	cttcctaata	aagttgaaat
16201	tacgcgtaaa	acagaattat	gatttaaadc	ttcaatttca	tcaatgtcaa	catcataaaa
16261	tgaaatttca	ttttctgttc	tatcaaataa	cgctatacat	aaacttccat	tcttaaaacg
16321	aaaaacatgc	ttcaactcaa	tgttttttgt	ttcattttcc	atttttgtta	ctccttgttt
16381	tgattacata	cttagtatag	caaacgttta	aaagttttgt	caatagtttt	tcttaaaaaa
16441	gtttaaataa	ttttaaaact	actatttaat	agaagaaata	agatttttaag	ttcaaatacat
16501	aattttgaat	aaaagtcaat	agatacataa	attttgtatt	tgatgaatat	gtaatagggt
16561	agataagttg	gttaagttgt	tgacacagtat	ttttaagttt	agtaaagaaa	tgataagtaa
16621	atttataagt	tttgattttgt	ataatcgttt	attttaaacc	ggtggggt	

TABLE 2

1st position (5' end)	2nd position				3rd position (3' end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

TABLE 3

44AHJDORF012, Nucleotides and amino acids sequences

8391 atgaacgaagtaaaattcagattttacagactcagaagcgtttcac
 1 M N E V K F R F T D S E A F H
 8436 atgtttatatacgtggtggttttaaaattactctactttttattt
 16 M F I Y A G D L K L L Y F L F
 8481 gtattaatgttcgttgatattattacaggtattttcaaaagcaatt
 31 V L M F V D I I T G I S K A I
 8526 aaaaaataaacttatgggtcaaaaaaatcaatgagaggattttct
 46 K N N N L W S K K S M R G F S
 8571 aaaaaattattgatattctgtattatcatttttagcaaaccatt
 61 K K L L I F C I I I L A N I I
 8616 gaccagattttacaattaaaagggtggtctactcatgattacaata
 76 D Q I L Q L K G G L L M I T I
 8661 ttttattatattgcaaattgagggactttctattgtagaaaattgt
 91 F Y Y I A N E G L S I V E N C
 8706 gcagaaatggacgtatttagtaccagaacaaattaaagataaatta
 106 A E M D V L V P E Q I K D K L
 8751 agagtcattaaaaatgatactgaaaagagtgataacaatgaacga
 121 R V I K N D T E K S D N N E R
 8796 tcaagagaagatagataa 8813
 136 S R E D R *

44AHJDORF025, Nucleotides and amino acids sequences

15175 atggaacgtaaatacaaaaacggtattattatattgcatgagatt
 1 M E R K Y K T V L L Y C D E I
 15130 aaaggacattttccacatcaaattctcaatgtttgaagatttatat
 16 K G H F P H Q I S M F E D L Y
 15085 gacgctaaagttgtatattcatattatgaatataacctgttcact
 31 D A K V V Y S Y Y E Y N L F T
 15040 aaaaaatacgcgtatatcatagaatacattaaggagatataa 14999
 46 K K Y A Y I I E Y I K E I *

TABLE 4

Similarities with public sequences

Query= pt|110882 44AHJDORF012 44AHJD_NT|8391-8813|3 1
(140 letters)

Database: nr
445,337 sequences; 137,034,979 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 140528 sp P24811 YQXH_BACSU HYPOTHETICAL 15.7 KD PROTEIN IN ...	80	6e-15
gi 4126631 dbj BAA36651.1 (AB016282) ORF45 [bacteriophage phi-...	76	1e-13
gi 141088 sp P26835 YNGD_CLOPE HYPOTHETICAL 14.9 KD PROTEIN IN ...	61	5e-09
gi 2293160 (AF008220) YtkC [Bacillus subtilis] >gi 2635548 emb ...	36	0.11
gi 1181973 emb CAA87743.1 (Z47794) holin protein [Bacteriophag...	31	3.8
gi 4981272 gb AAD35828.1 AE001744_18 (AE001744) carboxyl-termin...	30	8.5

Query= pt|110882 44AHJDORF012 44AHJD_NT|8391-8813|3 1
(140 letters)

Database: swissprot
83,367 sequences; 30,300,539 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P24811 YQXH_BACSU HYPOTHETICAL 15.7 KD PROTEIN IN SPOIIC-C...	80	2e-15
sp P26835 YNGD_CLOPE HYPOTHETICAL 14.9 KD PROTEIN IN NAGH 3'RE...	61	1e-09
sp P18015 COP_CLOPE COPY NUMBER PROTEIN (ORF4).	28	7.9

Query= pt|110899 44AHJDORF025 44AHJD_NT|14999-15175|-3 1
(58 letters)

Database: nr
445,337 sequences; 137,034,979 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 1706558 sp P52869 EAEA_HAFAL INTIMIN (OUTER MEMBRANE PROTEIN...	28	8.4

Query= pt|110899 44AHJDORF025 44AHJD_NT|14999-15175|-3 1
(58 letters)

Database: swissprot
83,367 sequences; 30,300,539 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P52869 EAEA_HAFAL INTIMIN (OUTER MEMBRANE PROTEIN) (ATTACHI...	28	1.9
sp Q02785 PDRC_YEAST ATP-DEPENDENT PERMEASE PDR12.	27	4.2
sp P75252 Y350_MYCPN HYPOTHETICAL PROTEIN MG350 HOMOLOG.	27	5.6
sp P41665 Y112_NPVAC HYPOTHETICAL 10.5 KD PROTEIN IN HE65-PK2 ...	27	5.6
sp P26744 VG01_BPP22 PORTAL PROTEIN (PROTEIN GPI).	26	7.3
sp P36542 ATPG_HUMAN ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL P...	26	9.5
sp P35435 ATPG_RAT ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL (EC...	26	9.5

TABLE 5

Physico-chemical parameters for 44AHJDORF012

1 MNEVKFRFTD SEAFHMFIIYA GDLKLLYFLF VLMFVDIITG ISKAIKNNNL WSKKSMRGFS
61 KKLLIFCIII LANIIDQILQ LKGGLLMITI FYYIANEGLS IVENCAEMDV LVPEQIKDKL
121 RVIKNDTEKS DNNERSREDR

Number of amino acids: 140
Average molecular weight (Daltons): 16294.30
Mean amino acid weight (Daltons): 116.39
Monoisotopic molecular weight (Daltons): 16283.58
Mean amino acid monoisotopic weight (Daltons): 116.31

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	6	4.29%	7.58%	Cys	C	2	1.43%	1.66%
Asp	D	9	6.43%	5.28%	Glu	E	9	6.43%	6.37%
Phe	F	10	7.14%	4.09%	Gly	G	6	4.29%	6.84%
His	H	1	0.71%	2.24%	Ile	I	18	12.86%	5.81%
Lys	K	13	9.29%	5.95%	Leu	L	16	11.43%	9.42%
Met	M	6	4.29%	2.37%	Asn	N	10	7.14%	4.45%
Pro	P	1	0.71%	4.9%	Gln	Q	3	2.14%	3.97%
Arg	R	6	4.29%	5.16%	Ser	S	8	5.71%	7.12%
Thr	T	4	2.86%	5.67%	Val	V	7	5.00%	6.58%
Trp	W	1	0.71%	1.23%	Tyr	Y	4	2.86%	3.18%

Number of acidic (negative) amino acids (ED): 18 12.86%
Number of basic (positive) amino acids (KR): 19 13.57%
Total charge (KRED): 37 26.43%
Net charge (KR - ED): 1 0.71%
Theoretical pI: 8.16
Total linear charge density: 0.28

Average hydrophobicity: 1.26
Ratio of hydrophilicity to hydrophobicity: 0.92
Percentage of hydrophilic amino acid: 45.71%
Percentage of hydrophobic amino acid: 54.29%
Ratio of %hydrophilic to %hydrophobic: 0.84

Hydrophobicity plot

Kyte-Doolittle scale

Ala: 1.800 Arg: -4.500 Asn: -3.500
Asp: -3.500 Cys: 2.500 Gly: -0.400
Gln: -3.500 Glu: -3.500 His: -3.200
Ile: 4.500 Leu: 3.800 Lys: -3.900
Met: 1.900 Phe: 2.800 Pro: -1.600
Ser: -0.800 Thr: -0.700 Trp: -0.900
Tyr: -1.300 Val: 4.200

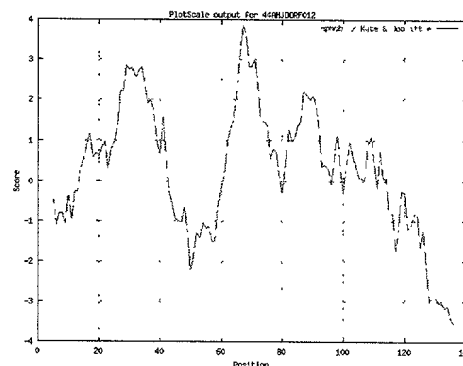


TABLE 5

Physico-chemical parameters for 44AHJDORF025

1 MERKYKTVLL YCDEIKGHFP HQISMFEPLY DAKVVYSYYE YNLFTKKYAY IIEYIKEI

Number of amino acids: 58
 Average molecular weight (Daltons): 7248.41
 Mean amino acid weight (Daltons): 124.97
 Monoisotopic molecular weight (Daltons): 7243.60
 Mean amino acid monoisotopic weight (Daltons): 124.89

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	2	3.45%	7.58%	Cys	C	1	1.72%	1.66%
Asp	D	3	5.17%	5.28%	Glu	E	6	10.34%	6.37%
Phe	F	3	5.17%	4.09%	Gly	G	1	1.72%	6.84%
His	H	2	3.45%	2.24%	Ile	I	6	10.34%	5.81%
Lys	K	7	12.07%	5.95%	Leu	L	4	6.90%	9.42%
Met	M	2	3.45%	2.37%	Asn	N	1	1.72%	4.45%
Pro	P	1	1.72%	4.9%	Gln	Q	1	1.72%	3.97%
Arg	R	1	1.72%	5.16%	Ser	S	2	3.45%	7.12%
Thr	T	2	3.45%	5.67%	Val	V	3	5.17%	6.58%
Trp	W	0	0.00%	1.23%	Tyr	Y	10	17.24%	3.18%

Number of acidic (negative) amino acids (ED): 9 15.52%
 Number of basic (positive) amino acids (KR): 8 13.79%
 Total charge (KRED): 17 29.31%
 Net charge (KR - ED): -1 -1.72%
 Theoretical pI: 6.08
 Total linear charge density: 0.33

Average hydrophobicity: -3.72
 Ratio of hydrophilicity to hydrophobicity: 1.30
 Percentage of hydrophilic amino acid: 44.83%
 Percentage of hydrophobic amino acid: 55.17%
 Ratio of %hydrophilic to %hydrophobic: 0.81

Hydrophobicity plot

Kyte-Doolittle scale

Ala: 1.800 Arg: -4.500 Asn: -3.500
 Asp: -3.500 Cys: 2.500 Gly: -0.400
 Gln: -3.500 Glu: -3.500 His: -3.200
 Ile: 4.500 Leu: 3.800 Lys: -3.900
 Met: 1.900 Phe: 2.800 Pro: -1.600
 Ser: -0.800 Thr: -0.700 Trp: -0.900
 Tyr: -1.300 Val: 4.200

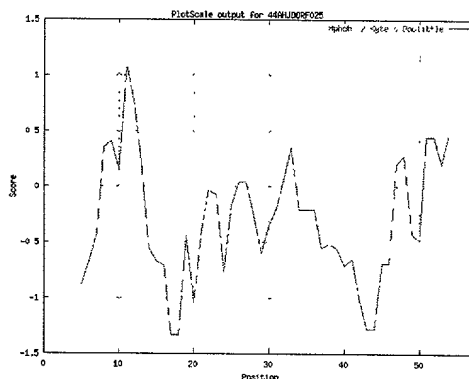


TABLE 6

>gi|11094395|gb|AAG29618.1| integrase-like protein [Staphylococcus aureus]
>gi|11094394|gb|AAG29617.1|AF217235_20 Orf20 [Staphylococcus aureus]
>gi|11094393|gb|AAG29616.1|AF217235_19 Orf19 [Staphylococcus aureus]
>gi|11094392|gb|AAG29615.1|AF217235_18 Orf18 [Staphylococcus aureus]
>gi|11094391|gb|AAG29614.1|AF217235_17 Orf17 [Staphylococcus aureus]
>gi|11094390|gb|AAG29613.1|AF217235_16 Orf16 [Staphylococcus aureus]
>gi|11094389|gb|AAG29612.1|AF217235_15 Orf15 [Staphylococcus aureus]
>gi|11094388|gb|AAG29611.1|AF217235_14 Orf14 [Staphylococcus aureus]
>gi|11094387|gb|AAG29610.1|AF217235_13 Orf13 [Staphylococcus aureus]
>gi|11094386|gb|AAG29609.1|AF217235_12 Orf12 [Staphylococcus aureus]
>gi|11094385|gb|AAG29608.1|AF217235_11 Orf11 [Staphylococcus aureus]
>gi|11094384|gb|AAG29607.1|AF217235_10 Orf10 [Staphylococcus aureus]
>gi|11094383|gb|AAG29606.1|AF217235_9 Orf9 [Staphylococcus aureus]
>gi|11094382|gb|AAG29605.1|AF217235_8 Orf8 [Staphylococcus aureus]
>gi|11094381|gb|AAG29604.1|AF217235_7 Orf7 [Staphylococcus aureus]
>gi|11094380|gb|AAG29603.1|AF217235_6 Orf6 [Staphylococcus aureus]
>gi|11094379|gb|AAG29602.1|AF217235_5 Orf5 [Staphylococcus aureus]
>gi|11094378|gb|AAG29601.1|AF217235_4 toxic shock syndrome toxin-1 [Staphylococcus aureus]
>gi|11094377|gb|AAG29600.1|AF217235_3 Orf3 [Staphylococcus aureus]
>gi|11094376|gb|AAG29599.1|AF217235_2 staphylococcal enterotoxin C-bovine [Staphylococcus aureus]
>gi|11094375|gb|AAG29598.1|AF217235_1 sel [Staphylococcus aureus]
>gi|9944978|gb|AAG03058.1|AF288215_5 response regulator [Staphylococcus aureus]
>gi|9944977|gb|AAG03057.1|AF288215_4 receptor histidine kinase [Staphylococcus aureus]
>gi|9944976|gb|AAG03056.1|AF288215_3 Agr autoinducing peptide precursor [Staphylococcus aureus]
>gi|9944975|gb|AAG03055.1|AF288215_2 putative AIP processing-secretion protein [Staphylococcus aureus]
>gi|9944974|gb|AAG03054.1|AF288215_1 delta hemolysin [Staphylococcus aureus]
>gi|10956173|ref|NP_048342.1| ORF64 [Staphylococcus aureus]
>gi|10956172|ref|NP_048341.1| replication protein [Staphylococcus aureus]
>gi|10956170|ref|NP_048340.1| ORF64 [Staphylococcus aureus]
>gi|10956169|ref|NP_048339.1| replication protein [Staphylococcus aureus]
>gi|10956167|ref|NP_052696.1| pot. orfB (aa 1-92) (4557 is 2nd base in codon) [Staphylococcus aureus]
>gi|10956166|ref|NP_052695.1| pot. orfA [Staphylococcus aureus]
>gi|10956165|ref|NP_052694.1| CAT gene (aa 1-215) [Staphylococcus aureus]
>gi|10956164|ref|NP_052693.1| repD (aa 1-311) [Staphylococcus aureus]
>gi|10956163|ref|NP_052692.1| unidentified reading frame [Staphylococcus aureus]
>gi|10956161|ref|NP_052691.1| kanamycin nucleotidyltransferase (AA 1-253) [Staphylococcus aureus]
>gi|10956160|ref|NP_052690.1| repB polypeptide (AA 1-235) [Staphylococcus aureus]
>gi|10956158|ref|NP_052168.1| recombination protein [Staphylococcus aureus]
>gi|10956157|ref|NP_052167.1| CAT protein [Staphylococcus aureus]
>gi|10956156|ref|NP_052166.1| replication protein [Staphylococcus aureus]
>gi|10956154|ref|NP_053794.1| replication protein [Staphylococcus aureus]
>gi|10956153|ref|NP_053796.1| recombination protein [Staphylococcus aureus]
>gi|10956152|ref|NP_053795.1| tetracycline resistance protein [Staphylococcus aureus]
>gi|10956150|ref|NP_052130.1| beta-lactamase [Staphylococcus aureus]
>gi|10956148|ref|NP_052129.1| beta-lactamase [Staphylococcus aureus]
>gi|10956146|ref|NP_044360.1| tetracycline resistance protein [Staphylococcus aureus]
>gi|10956145|ref|NP_044359.1| replication protein [Staphylococcus aureus]
>gi|10956143|ref|NP_040438.1| reading frame D [Staphylococcus aureus]
>gi|10956142|ref|NP_040437.1| CAT (chloramphenicol resistance) [Staphylococcus aureus]
>gi|10956141|ref|NP_040435.1| reading frame A [Staphylococcus aureus]
>gi|10956140|ref|NP_040436.1| reading frame C (replication) [Staphylococcus aureus]
>gi|10946545|gb|AAG23889.1| TcaB [Staphylococcus aureus]
>gi|10946544|gb|AAG23888.1| TcaA [Staphylococcus aureus]
>gi|10946543|gb|AAG23887.1| TcaR [Staphylococcus aureus]
>gi|2792490|gb|AAB97073.1| coenzyme A disulfide reductase [Staphylococcus aureus]
>gi|10835501|pdb|1D2P|A Chain A, Crystal Structure Of Two B Repeat Units (B1b2) Of The Collagen Binding Protein (Cna) Of Staphylococcus Aureus
>gi|10835500|pdb|1D2O|B Chain B, Crystal Structure Of A Single B Repeat Unit (B1) Of Collagen Binding Surface Protein (Cna) Of Staphylococcus Aureus.
>gi|10835499|pdb|1D2O|A Chain A, Crystal Structure Of A Single B Repeat Unit (B1) Of Collagen Binding Surface Protein (Cna) Of Staphylococcus Aureus.
>gi|1169372|sp|P45555|DNAJ_STAAU CHAPERONE PROTEIN DNAJ (HSP40)
>gi|7672995|gb|AAF66692.1|AF144682_1 immunodominant antigen B [Staphylococcus aureus]
>gi|7672993|gb|AAF66691.1|AF144681_1 immunodominant antigen A [Staphylococcus aureus]
>gi|9955268|pdb|1QE0|B Chain B, Crystal Structure Of Apo S. Aureus Histidyl-Trna Synthetase
>gi|9955267|pdb|1QE0|A Chain A, Crystal Structure Of Apo S. Aureus Histidyl-Trna Synthetase

>gi|9955226|pdb|1F77|B Chain B, Staphylococcal Enterotoxin H Determined To 2.4 A Resolution
>gi|9955225|pdb|1F77|A Chain A, Staphylococcal Enterotoxin H Determined To 2.4 A Resolution
>gi|9954962|pdb|1C79|B Chain B, Staphylokinase (Sak) Dimer
>gi|9954961|pdb|1C79|A Chain A, Staphylokinase (Sak) Dimer
>gi|9954960|pdb|1C78|B Chain B, Staphylokinase (Sak) Dimer
>gi|9954959|pdb|1C78|A Chain A, Staphylokinase (Sak) Dimer
>gi|9954958|pdb|1C77|B Chain B, Staphylokinase (Sak) Dimer
>gi|9954957|pdb|1C77|A Chain A, Staphylokinase (Sak) Dimer
>gi|9954956|pdb|1C76|A Chain A, Staphylokinase (Sak) Monomer
>gi|9954208|gb|AAG08983.1|AF186237_1 ABC protein VgaA variant [Staphylococcus aureus]
>gi|9937366|gb|AAG02426.1|AF290087_3 phosphomevalonate kinase [Staphylococcus aureus]
>gi|9937365|gb|AAG02425.1|AF290087_2 mevalonate diphosphate decarboxylase [Staphylococcus aureus]
>gi|9937364|gb|AAG02424.1|AF290087_1 mevalonate kinase [Staphylococcus aureus]
>gi|9937362|gb|AAG02423.1|AF290086_2 HMG-CoA reductase [Staphylococcus aureus]
>gi|9937361|gb|AAG02422.1|AF290086_1 HMG-CoA synthase [Staphylococcus aureus]
>gi|7415524|dbj|BAA93438.1| FmtB [Staphylococcus aureus]
>gi|7415419|dbj|BAA93431.1| ORF1 [Staphylococcus aureus]
>gi|7415418|dbj|BAA93430.1| FmtB [Staphylococcus aureus]
>gi|10121057|pdb|1FFY|A Chain A, Insights Into Editing From An Ile-Trna Synthetase Structure With Trna(Ile) And Mupirocin
>gi|10041543|emb|CAC07605.1| unnamed protein product [Staphylococcus aureus]
>gi|1346939|sp|P23215|QACA_STAAU ANTISEPTIC RESISTANCE PROTEIN
>gi|119116|sp|P14319|QACC_STAAU QUATERNARY AMMONIUM COMPOUND-RESISTANCE PROTEIN QACC (QUATERNARY AMMONIUM DETERMINANT C) (ETHIDIUM BROMIDE RESISTANCE PROTEIN) (MULTIDRUG RESISTANCE PROTEIN)
>gi|9971595|dbj|BAB12579.1| coagulase [Staphylococcus aureus]
>gi|9971593|dbj|BAB12578.1| coagulase [Staphylococcus aureus]
>gi|9971591|dbj|BAB12577.1| coagulase [Staphylococcus aureus]
>gi|9965494|gb|AAG02249.1| peptide deformylase Pdf1 [Staphylococcus aureus]
>gi|9931634|gb|AAG02239.1|AF295601_1 serine protease-like exoprotein E [Staphylococcus aureus]
>gi|9931632|gb|AAG02238.1|AF295600_1 serine protease-like exoprotein A [Staphylococcus aureus]
>gi|2494147|sp|O05338|PRIM_STAAU DNA PRIMASE
>gi|2492884|sp|Q53634|MENE_STAAU O-SUCCINYLBENZOIC ACID--COA LIGASE (OSB-COA SYNTHETASE) (O-SUCCINYLBENZOATE-COA SYNTHASE)
>gi|1703465|sp|P52081|ATL_STAAU BIFUNCTIONAL AUTOLYSIN PRECURSOR [INCLUDES: N-ACETYLMURAMOYL-L-ALANINE AMIDASE ; MANNOSYL-GLYCOPROTEIN ENDO-BETA-N-ACETYLGLUCOSAMIDASE]
>gi|136130|sp|P19380|T431_STAAU TRANSPOSASE FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC
>gi|136126|sp|P14506|T257_STAAU TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS257 IN TRANSPOSON TN4003
>gi|113675|sp|P24556|ALYS_STAAU AUTOLYSIN (N-ACETYLMURAMOYL-L-ALANINE AMIDASE)
>gi|9801983|gb|AAF99572.1| replication initiation protein [Staphylococcus aureus]
>gi|9801982|gb|AAF99571.1| unknown [Staphylococcus aureus]
>gi|9801981|gb|AAF99570.1| recombinase [Staphylococcus aureus]
>gi|9801980|gb|AAF99569.1| MphBM [Staphylococcus aureus]
>gi|9801979|gb|AAF99568.1| erythromycin resistance protein [Staphylococcus aureus]
>gi|9801978|gb|AAF99567.1| transposase [Staphylococcus aureus]
>gi|9801977|gb|AAF99566.1| unknown [Staphylococcus aureus]
>gi|9801976|gb|AAF99565.1| unknown [Staphylococcus aureus]
>gi|9755015|gb|AAF98155.1|AF251216_3 FhuG [Staphylococcus aureus]
>gi|9755014|gb|AAF98154.1|AF251216_2 FhuB [Staphylococcus aureus]
>gi|9755013|gb|AAF98153.1|AF251216_1 FhuC [Staphylococcus aureus]
>gi|9743649|gb|AAF97986.1| unknown [Staphylococcus aureus]
>gi|9743648|gb|AAD33530.3|AF132117_7 unknown [Staphylococcus aureus]
>gi|9743647|gb|AAD33529.3|AF132117_6 unknown [Staphylococcus aureus]
>gi|9743646|gb|AAD33527.2|AF132117_4 FhuA [Staphylococcus aureus]
>gi|9743645|gb|AAD33526.3|AF132117_3 ferrichrome transport permease [Staphylococcus aureus]
>gi|9743644|gb|AAD33524.3|AF132117_1 ferrichrome transport permease [Staphylococcus aureus]
>gi|9739161|gb|AAF97930.1|AF271715_6 serine protease SplF [Staphylococcus aureus]
>gi|9739160|gb|AAF97929.1|AF271715_5 serine protease SplE [Staphylococcus aureus]
>gi|9739159|gb|AAF97928.1|AF271715_4 serine protease SplD [Staphylococcus aureus]
>gi|9739158|gb|AAF97927.1|AF271715_3 serine protease SplC [Staphylococcus aureus]
>gi|9739157|gb|AAF97926.1|AF271715_2 serine protease SplB [Staphylococcus aureus]
>gi|9739156|gb|AAF97925.1|AF271715_1 serine protease SplA [Staphylococcus aureus]
>gi|9711569|dbj|BAB07846.1| coagulase [Staphylococcus aureus]
>gi|9711565|dbj|BAB07845.1| coagulase [Staphylococcus aureus]
>gi|9711561|dbj|BAB07844.1| coagulase [Staphylococcus aureus]
>gi|9711557|dbj|BAB07843.1| coagulase [Staphylococcus aureus]
>gi|9711553|dbj|BAB07842.1| coagulase [Staphylococcus aureus]
>gi|9711549|dbj|BAB07841.1| coagulase [Staphylococcus aureus]
>gi|9711545|dbj|BAB07840.1| coagulase [Staphylococcus aureus]
>gi|9711541|dbj|BAB07839.1| coagulase [Staphylococcus aureus]
>gi|9711537|dbj|BAB07838.1| coagulase [Staphylococcus aureus]

>gi|9711533|dbj|BAB07837.1| coagulase [Staphylococcus aureus]
>gi|9711528|dbj|BAB07836.1| coagulase [Staphylococcus aureus]
>gi|9711524|dbj|BAB07835.1| coagulase [Staphylococcus aureus]
>gi|9711520|dbj|BAB07834.1| coagulase [Staphylococcus aureus]
>gi|9711516|dbj|BAB07833.1| coagulase [Staphylococcus aureus]
>gi|9711512|dbj|BAB07832.1| coagulase [Staphylococcus aureus]
>gi|9711508|dbj|BAB07831.1| coagulase [Staphylococcus aureus]
>gi|9711504|dbj|BAB07830.1| coagulase [Staphylococcus aureus]
>gi|9711500|dbj|BAB07829.1| coagulase [Staphylococcus aureus]
>gi|9711496|dbj|BAB07828.1| coagulase [Staphylococcus aureus]
>gi|9711492|dbj|BAB07827.1| coagulase [Staphylococcus aureus]
>gi|9711488|dbj|BAB07826.1| coagulase [Staphylococcus aureus]
>gi|9711484|dbj|BAB07825.1| coagulase [Staphylococcus aureus]
>gi|9711480|dbj|BAB07824.1| coagulase [Staphylococcus aureus]
>gi|9622622|gb|AAF89877.1| putative site-specific recombinase XerC [Staphylococcus aureus]
>gi|9622620|gb|AAF89876.1| putative site-specific recombinase XerD [Staphylococcus aureus]
>gi|3806109|gb|AAC69195.1| HsdM-like protein [Staphylococcus aureus]
>gi|3806108|gb|AAC69194.1| exotoxin 4 [Staphylococcus aureus]
>gi|3806107|gb|AAC69193.1| exotoxin 5 [Staphylococcus aureus]
>gi|3806106|gb|AAC69192.1| exotoxin 1 [Staphylococcus aureus]
>gi|3806105|gb|AAC69191.1| exotoxin 3 [Staphylococcus aureus]
>gi|3806104|gb|AAC69190.1| exotoxin 2 [Staphylococcus aureus]
>gi|6176434|gb|AAF05589.1|AF188837_1 exotoxin 1 [Staphylococcus aureus]
>gi|6176433|gb|AAF05588.1|AF188836_1 exotoxin 1 [Staphylococcus aureus]
>gi|6176432|gb|AAF05587.1|AF188835_1 exotoxin 1 [Staphylococcus aureus]
>gi|9501795|dbj|BAB03342.1| Protein A [Staphylococcus aureus]
>gi|9501794|dbj|BAB03341.1| hypothetical protein [Staphylococcus aureus]
>gi|9501793|dbj|BAB03340.1| hypothetical protein [Staphylococcus aureus]
>gi|9501791|dbj|BAB03339.1| ABC transporter [Staphylococcus aureus]
>gi|9501790|dbj|BAB03338.1| ABC transporter [Staphylococcus aureus]
>gi|9501788|dbj|BAB03337.1| ABC transporter [Staphylococcus aureus]
>gi|9501787|dbj|BAB03336.1| ABC transporter [Staphylococcus aureus]
>gi|9501785|dbj|BAB03335.1| hypothetical protein [Staphylococcus aureus]
>gi|9501784|dbj|BAB03334.1| hypothetical protein [Staphylococcus aureus]
>gi|9501783|dbj|BAB03333.1| hypothetical protein [Staphylococcus aureus]
>gi|9501781|dbj|BAB03332.1| fructose specific permease [Staphylococcus aureus]
>gi|9501780|dbj|BAB03331.1| fructose 1-phosphate kinase [Staphylococcus aureus]
>gi|9501779|dbj|BAB03330.1| fru operon repressor [Staphylococcus aureus]
>gi|9501777|dbj|BAB03329.1| hypothetical protein [Staphylococcus aureus]
>gi|9501776|dbj|BAB03328.1| acetyl-CoA c-acetyltransferase [Staphylococcus aureus]
>gi|9501775|dbj|BAB03327.1| long chain fatty acid CoA ligase [Staphylococcus aureus]
>gi|9501774|dbj|BAB03326.1| Pro/Bet transporter homolog [Staphylococcus aureus]
>gi|9501772|dbj|BAB03325.1| response regulator [Staphylococcus aureus]
>gi|9501771|dbj|BAB03324.1| histidine kinase sensor [Staphylococcus aureus]
>gi|9501770|dbj|BAB03323.1| hypothetical protein [Staphylococcus aureus]
>gi|9501769|dbj|BAB03322.1| hypothetical protein [Staphylococcus aureus]
>gi|9501768|dbj|BAB03321.1| methionin aminopeptidase [Staphylococcus aureus]
>gi|9501767|dbj|BAB03320.1| hypothetical protein [Staphylococcus aureus]
>gi|7328282|emb|CAB82465.1| catabolite control protein A [Staphylococcus aureus]
>gi|9408171|emb|CAA71131.1| ORF213 [Staphylococcus aureus]
>gi|9408170|emb|CAA71130.1| ORF133 [Staphylococcus aureus]
>gi|9408169|emb|CAA71129.1| aldehyde dehydrogenase [Staphylococcus aureus]
>gi|8895763|gb|AAF81096.1|AF228662_1 putative undecaprenol kinase [Staphylococcus aureus]
>gi|8777467|dbj|BAA97049.1| 29-kDa cell surface protein [Staphylococcus aureus]
>gi|7328286|emb|CAB82467.1| diaminopimelate decarboxylase [Staphylococcus aureus]
>gi|581546|emb|CAA36783.1| AgrB protein [Staphylococcus aureus]
>gi|581545|emb|CAA36781.1| hypothetical protein [Staphylococcus aureus]
>gi|46600|emb|CAA37901.1| putative transposase [Staphylococcus aureus]
>gi|46599|emb|CAA37900.1| putative transposase [Staphylococcus aureus]
>gi|46513|emb|CAA36786.1| hypothetical protein [Staphylococcus aureus]
>gi|46512|emb|CAA36785.1| hypothetical protein [Staphylococcus aureus]
>gi|46511|emb|CAA36784.1| AgrA protein [Staphylococcus aureus]
>gi|46509|emb|CAA36782.1| hypothetical protein [Staphylococcus aureus]
>gi|46507|emb|CAA36780.1| Hld protein [Staphylococcus aureus]
>gi|46506|emb|CAA36779.1| hypothetical protein [Staphylococcus aureus]
>gi|9256926|pdb|1D6E|C Chain C, Crystal Structure Of Hla-Dr4 Complex With Peptidomimetic And Seb
>gi|9256923|pdb|1D5Z|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Peptidomimetic And Seb
>gi|9256920|pdb|1D5X|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Dipeptide Mimetic And Seb
>gi|9256852|pdb|1D5M|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Peptide And Seb

>gi|8569412|pdb|1DEE|H Chain H, Crystal Structure At 2.7a Resolution Of A Complex Between A Staphylococcus Aureus Domain And A Fab Fragment Of A Human Igm Antibody
>gi|8569411|pdb|1DEE|G Chain G, Crystal Structure At 2.7a Resolution Of A Complex Between A Staphylococcus Aureus Domain And A Fab Fragment Of A Human Igm Antibody
>gi|9246437|gb|AAF86053.1|AF210139_1 fmtA-like protein [Staphylococcus aureus]
>gi|9230553|gb|AAF85897.1|AF165314_2 putative protein histidine kinase ArlS [Staphylococcus aureus]
>gi|9230552|gb|AAF85896.1|AF165314_1 putative response regulator ArlR [Staphylococcus aureus]
>gi|9181843|gb|AAF85653.1|orfX [Staphylococcus aureus]
>gi|9181842|gb|AAF85652.1|orf1260 [Staphylococcus aureus]
>gi|9181841|gb|AAF85651.1|AF181950_8 transposase [Staphylococcus aureus]
>gi|9181840|gb|AAF85650.1|AF181950_7 alpha protein [Staphylococcus aureus]
>gi|9181839|gb|AAF85649.1|AF181950_6 beta protein [Staphylococcus aureus]
>gi|9181838|gb|AAF85648.1|AF181950_5 bleomycin resistance protein [Staphylococcus aureus]
>gi|9181837|gb|AAF85647.1|AF181950_4 kanamycin resistance protein [Staphylococcus aureus]
>gi|9181836|gb|AAF85646.1|AF181950_3 transposase [Staphylococcus aureus]
>gi|9181835|gb|AAF85645.1|AF181950_1 low affinity penicillin binding protein [Staphylococcus aureus]
>gi|3603441|gb|AAC35853.1|type b beta-lactamase [Staphylococcus aureus]
>gi|8928563|sp|P81177|AURE_STAAU ZINC METALLOPROTEINASE AUREOLYSIN PRECURSOR (STAPHYLOCOCCUS AUREUS NEUTRAL PROTEINASE)
>gi|9049372|dbj|BAA99412.1|exfoliative toxin C [Staphylococcus aureus]
>gi|2495148|sp|Q53727|PCRA_STAAU ATP-DEPENDENT DNA HELICASE PCRA
>gi|115038|sp|P00807|BLAC_STAAU BETA-LACTAMASE PRECURSOR (PENICILLINASE)
>gi|3724158|emb|CAA06500.1|lipoprotein [Staphylococcus aureus]
>gi|3724157|emb|CAA06499.1|ATP binding protein [Staphylococcus aureus]
>gi|3724156|emb|CAA06498.1|membrane protein [Staphylococcus aureus]
>gi|3724155|emb|CAA06497.1|membrane protein [Staphylococcus aureus]
>gi|8885990|gb|AAF80331.1|enterotoxin I [Staphylococcus aureus]
>gi|8648965|emb|CAB94853.1|Map-ND2C protein [Staphylococcus aureus]
>gi|8569359|pdb|1EWC|A Chain A, Crystal Structure Of Zn2+ Loaded Staphylococcal Enterotoxin H
>gi|8134803|sp|Q9ZEH3|UVRC_STAAU EXCINUCLEASE ABC SUBUNIT C
>gi|8134747|sp|Q9Z5C3|TPIS_STAAU TRIOSEPHOSPHATE ISOMERASE (TIM)
>gi|8134611|sp|Q9Z5C4|PGK_STAAU PHOSPHOGLYCERATE KINASE
>gi|8134576|sp|O86491|MURE_STAAU UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIPELATE LIGASE (UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE) (MESO-DIAMINOPIPELATE-ADDING ENZYME) (UDP-MURNAC-TRIPETIDE SYNTHETASE)
>gi|7674177|sp|Q9ZAG8|RECU_STAAU RECOMBINATION PROTEIN U HOMOLOG (PENICILLIN-BINDING PROTEIN-RELATED FACTOR A HOMOLOG) (PBP RELATED FACTOR A HOMOLOG)
>gi|7674147|sp|Q9Z5C9|NRDI_STAAU NRDI PROTEIN
>gi|7388052|sp|O86490|RF3_STAAU PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3)
>gi|7387927|sp|Q9ZEH5|MUS2_STAAU MUTS2 PROTEIN
>gi|7227940|sp|P95842|RSBV_STAAU ANTI-SIGMA B FACTOR ANTAGONIST
>gi|6920067|sp|P81683|EFG_STAAU ELONGATION FACTOR G (EF-G) (85 KDA VITRONECTIN BINDING PROTEIN)
>gi|6686369|sp|O32418|APT_STAAU ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)
>gi|6685442|sp|P56740|FOLB_STAAU DIHYDRONEOPTERIN ALDOLASE (DHNA)
>gi|6651452|gb|AAF22306.1|AF189239_1 repressor of toxins Rot [Staphylococcus aureus]
>gi|6647733|sp|O32419|RELA_STAAU GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) ((P)PPGPP SYNTHETASE)
>gi|6647411|sp|Q9ZAH5|ALR_STAAU ALANINE RACEMASE
>gi|6226944|sp|O07322|MRAY_STAAU PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (UDP-MURNAC-PENTAPEPTIDE PHOSPHOTRANSFERASE)
>gi|6226498|sp|O05337|YSI3_STAAU HYPOTHETICAL 30.4 KDA PROTEIN IN SIGMA70 OPERON (ORF30)
>gi|6225004|sp|Q9ZAH6|ACPS_STAAU HOLO-[ACYL-CARRIER PROTEIN] SYNTHASE (HOLO-ACP SYNTHASE)
>gi|3913884|sp|Q59801|HYSA_STAAU HYALURONATE LYASE PRECURSOR (HYALURONIDASE) (HYASE)
>gi|3122409|sp|O33595|MURD_STAAU UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE (UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMATE SYNTHETASE) (D-GLUTAMIC ACID ADDING ENZYME)
>gi|3122408|sp|O31211|MURC_STAAU UDP-N-ACETYLMURAMATE--ALANINE LIGASE (UDP-N-ACETYLMURAMOYL-L-ALANINE SYNTHETASE)
>gi|2500720|sp|O06446|SECA_STAAU PREPROTEIN TRANSLOCASE SECA SUBUNIT
>gi|2499415|sp|Q59821|ODP2_STAAU DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX (E2)
>gi|2498749|sp|Q53726|PCRB_STAAU PCRB PROTEIN
>gi|2494749|sp|Q59812|GLNA_STAAU GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) (GS)
>gi|2492949|sp|Q59803|AROC_STAAU CHORISMATE SYNTHASE (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE)
>gi|1723227|sp|P52080|YAT3_STAAU HYPOTHETICAL 16.6 KDA PROTEIN IN ATL 5'REGION (ORF3)
>gi|1723225|sp|P52079|YAT2_STAAU HYPOTHETICAL 18.3 KDA PROTEIN IN ATL 5'REGION (ORF2)
>gi|1723223|sp|P52078|YAT1_STAAU HYPOTHETICAL PROTEIN IN ATL 5'REGION (ORF1)
>gi|1709887|sp|P51183|PT1_STAAU PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I)
>gi|1708172|sp|P50915|HEM2_STAAU DELTA-AMINOLEVULINIC ACID DEHYDRATASE (PORPHOBILINOGEN SYNTHASE) (ALAD) (ALADH)

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>gi|1174521|sp|P41972|SYI_STAAU ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
>gi|1172890|sp|Q02350|RECA_STAAU RECA PROTEIN
>gi|1170027|sp|P45553|GRPE_STAAU GRPE PROTEIN (HSP-70 COFACTOR) (HSP20)
>gi|729030|sp|P39862|CAPM_STAAU CAPM PROTEIN
>gi|729026|sp|P39858|CAPI_STAAU CAPI PROTEIN
>gi|586026|sp|P02976|SPA1_STAAU IMMUNOGLOBULIN G BINDING PROTEIN A PRECURSOR (IGG BINDING PROTEIN A)
>gi|584922|sp|Q08854|CH60_STAAU 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK
PROTEIN 60)
>gi|461535|sp|Q05615|AROA_STAAU 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (5-
ENOLPYRUVYL-SHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS)
>gi|400202|sp|P31024|LSPA_STAAU LIPOPROTEIN SIGNAL PEPTIDASE (PROLIPOPROTEIN SIGNAL PEPTIDASE)
(SIGNAL PEPTIDASE II) (SPASE II)
>gi|141181|sp|P03861|YP14_STAAU HYPOTHETICAL 14.6 KDA PROTEIN (READING FRAME C) (REPLICATION)
>gi|136616|sp|P13954|TYSY_STAAU THYMIDYLATE SYNTHASE (TS) (TSASE)
>gi|127193|sp|P02979|ERM2_STAAU RRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-
STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
>gi|125925|sp|P11100|LACD_STAAU TAGATOSE 1,6-DIPHOSPHATE ALDOLASE (TAGATOSE-BISPHOSPHATE ALDOLASE)
(D-TAGATOSE-1,6-BISPHOSPHATE ALDOLASE)
>gi|125922|sp|P11099|LACC_STAAU TAGATOSE-6-PHOSPHATE KINASE (PHOSPHOTAGATOKINASE)
>gi|125919|sp|P26592|LACB_STAAU GALACTOSE-6-PHOSPHATE ISOMERASE LACB SUBUNIT
>gi|123185|sp|P01506|HLD_STAAU DELTA-HEMOLYSIN PRECURSOR (DELTA-TOXIN)
>gi|120457|sp|P14738|FNBA_STAAU FIBRONECTIN-BINDING PROTEIN PRECURSOR (FNBP)
>gi|113525|sp|P21545|AGRB_STAAU ACCESSORY GENE REGULATOR PROTEIN B
>gi|8101860|gb|AAF72664.1|AF259960_1 major cold shock protein CspA [Staphylococcus aureus]
>gi|8099634|gb|AAF72185.1|AF255950_1 AgrD signal peptide precursor [Staphylococcus aureus]
>gi|7959131|dbj|BAA95959.1| secretory protein SAI-B [Staphylococcus aureus]
>gi|7670327|dbj|BAA95014.1| TagG homolog [Staphylococcus aureus]
>gi|7670326|dbj|BAA95013.1| TagH homolog [Staphylococcus aureus]
>gi|7670325|dbj|BAA95012.1| TagA homolog [Staphylococcus aureus]
>gi|7670324|dbj|BAA95011.1| staphylokinase [Staphylococcus aureus]
>gi|7670323|dbj|BAA95010.1| hypothetical protein [Staphylococcus aureus]
>gi|7670322|dbj|BAA95009.1| KdpC homolog [Staphylococcus aureus]
>gi|7670321|dbj|BAA95008.1| KdpB homolog [Staphylococcus aureus]
>gi|7670320|dbj|BAA95007.1| KdpA homolog [Staphylococcus aureus]
>gi|7839534|gb|AAF70313.1|AF260326_2 SrrB [Staphylococcus aureus]
>gi|7839533|gb|AAF70312.1|AF260326_1 SrrA [Staphylococcus aureus]
>gi|7767013|pdb|1ENF|A Chain A, Crystal Structure Of Staphylococcal Enterotoxin H Determined To 1.69
A Resolution
>gi|3401995|pdb|2SPZ|A Chain A, Staphylococcal Protein A, Z-Domain, Nmr, 10 Structures
>gi|1280354|gb|AAA98144.1| ORFA [Staphylococcus aureus]
>gi|7594777|dbj|BAA82240.2| ORF CN050 [Staphylococcus aureus]
>gi|7594776|dbj|BAA82239.2| ORF CN049 [Staphylococcus aureus]
>gi|7594775|dbj|BAA82233.2| ORF N065 [Staphylococcus aureus]
>gi|7594774|dbj|BAA82227.2| ORF CN041 [Staphylococcus aureus]
>gi|7594773|dbj|BAA82226.2| ORF CN040 [Staphylococcus aureus]
>gi|7594772|dbj|BAA82223.2| ORF N060 [Staphylococcus aureus]
>gi|7594771|dbj|BAA82222.2| ORF CN038 [Staphylococcus aureus]
>gi|7594770|dbj|BAA94664.1| ORF N057 [Staphylococcus aureus]
>gi|7594769|dbj|BAA82219.2| methicillin resistance protein MecR1 [Staphylococcus aureus]
>gi|7594768|dbj|BAA82208.2| ORF N051 [Staphylococcus aureus]
>gi|7594767|dbj|BAA82207.2| ORF N050 [Staphylococcus aureus]
>gi|7594766|dbj|BAA82206.2| ORF N049 [Staphylococcus aureus]
>gi|7594765|dbj|BAA94663.1| ORF N043 [Staphylococcus aureus]
>gi|7594764|dbj|BAA94662.1| ORF N042 [Staphylococcus aureus]
>gi|7594763|dbj|BAA94661.1| ORF N041 [Staphylococcus aureus]
>gi|7594762|dbj|BAA94660.1| ORF N039 [Staphylococcus aureus]
>gi|7594761|dbj|BAA94659.1| ORF N038 [Staphylococcus aureus]
>gi|7594760|dbj|BAA94658.1| ORF N033 [Staphylococcus aureus]
>gi|7594759|dbj|BAA94657.1| ORF N032 [Staphylococcus aureus]
>gi|7594758|dbj|BAA94656.1| ORF N031 [Staphylococcus aureus]
>gi|7594757|dbj|BAA94655.1| ORF N030 [Staphylococcus aureus]
>gi|7594756|dbj|BAA94654.1| ORF N029 [Staphylococcus aureus]
>gi|7594755|dbj|BAA82191.2| ORF CN018 [Staphylococcus aureus]
>gi|7594754|dbj|BAA94653.1| ORF N024 [Staphylococcus aureus]
>gi|7594753|dbj|BAA82189.2| ORF CN017 [Staphylococcus aureus]
>gi|7594752|dbj|BAA82178.2| ORF CN007 [Staphylococcus aureus]
>gi|7594751|dbj|BAA94652.1| ORF N010 [Staphylococcus aureus]
>gi|7594750|dbj|BAA94651.1| ORF N009 [Staphylococcus aureus]
>gi|7594749|dbj|BAA94650.1| ORF N008 [Staphylococcus aureus]
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>gi|7594747|dbj|BAA82176.2| ORF CN005 [Staphylococcus aureus]
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>gi|7594743|dbj|BAA82173.2| ORF CN002 [Staphylococcus aureus]
>gi|7594742|dbj|BAA82171.2| ORF CN001 [Staphylococcus aureus]
>gi|7592634|dbj|BAA94340.1| hypothetical protein [Staphylococcus aureus]
>gi|7592633|dbj|BAA94339.1| hypothetical protein [Staphylococcus aureus]
>gi|7592632|dbj|BAA94338.1| hypothetical protein [Staphylococcus aureus]
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>gi|7592617|dbj|BAA94324.1| hypothetical protein [Staphylococcus aureus]
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>gi|7592608|dbj|BAA94316.1| hypothetical protein [Staphylococcus aureus]
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>gi|7592606|dbj|BAA94314.1| hypothetical protein [Staphylococcus aureus]
>gi|6332771|dbj|BAA86653.1| open reading frame X [Staphylococcus aureus]
>gi|6332770|dbj|BAA86652.1| transposase [Staphylococcus aureus]
>gi|6332769|dbj|BAA86651.1| glycerophosphoryl diester phosphodiesterase homologue [Staphylococcus aureus]
>gi|6332768|dbj|BAA86650.1| penicillin-binding protein 2' [Staphylococcus aureus]
>gi|6332767|dbj|BAA86649.1| hypothetical protein [Staphylococcus aureus]
>gi|6332766|dbj|BAA86648.1| cassette chromosome recombinase A1 [Staphylococcus aureus]
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>gi|6332762|dbj|BAA86644.1| hypothetical protein [Staphylococcus aureus]
>gi|6332759|dbj|BAA86641.1| hypothetical protein [Staphylococcus aureus]
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>gi|6332755|dbj|BAA86637.1| hypothetical protein [Staphylococcus aureus]
>gi|6332754|dbj|BAA86636.1| hypothetical protein [Staphylococcus aureus]
>gi|6332753|dbj|BAA86635.1| hypothetical protein [Staphylococcus aureus]
>gi|6332752|dbj|BAA86634.1| hypothetical protein [Staphylococcus aureus]
>gi|6332751|dbj|BAA86633.1| hypothetical protein [Staphylococcus aureus]
>gi|6332750|dbj|BAA86632.1| hypothetical protein [Staphylococcus aureus]
>gi|5360873|dbj|BAA82243.1| orfX [Staphylococcus aureus]
>gi|5360868|dbj|BAA82238.1| transposase for insertion sequence-like element IS431mec [Staphylococcus aureus]
>gi|5360864|dbj|BAA82234.1| plasmid recombination enzyme [Staphylococcus aureus]
>gi|5360860|dbj|BAA82230.1| bleomycin resistance protein(BRP) [Staphylococcus aureus]
>gi|5360859|dbj|BAA82229.1| kanamycin nucleotidyltransferase [Staphylococcus aureus]
>gi|5360858|dbj|BAA82228.1| transposase for insertion sequence-like element IS431mec [Staphylococcus aureus]
>gi|5360854|dbj|BAA82224.1| glycerophosphoryldiester phosphodiesterase [Staphylococcus aureus]
>gi|5360851|dbj|BAA82221.1| ORF N059 [Staphylococcus aureus]
>gi|5360850|dbj|BAA82220.1| penicillin binding protein 2' [Staphylococcus aureus]
>gi|5360848|dbj|BAA82218.1| methicillin resistance protein MecI [Staphylococcus aureus]
>gi|5360847|dbj|BAA82217.1| ORF CN035 [Staphylococcus aureus]
>gi|5360842|dbj|BAA82212.1| ORF CN032 [Staphylococcus aureus]
>gi|5360841|dbj|BAA82211.1| ORF N052 [Staphylococcus aureus]
>gi|5360840|dbj|BAA82210.1| ORF CN031 [Staphylococcus aureus]
>gi|5360839|dbj|BAA82209.1| ORF CN030 [Staphylococcus aureus]
>gi|5360835|dbj|BAA82205.1| rRNA adenine N-6-methyltransferase [Staphylococcus aureus]
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>gi|5360834|dbj|BAA82204.1| adenyltransferase(AAD9) [Staphylococcus aureus]
>gi|5360833|dbj|BAA82203.1| transposaseC [Staphylococcus aureus]
>gi|5360832|dbj|BAA82202.1| transposaseB [Staphylococcus aureus]
>gi|5360831|dbj|BAA82201.1| transposaseA [Staphylococcus aureus]
>gi|5360826|dbj|BAA82196.1| site-specific recombinase [Staphylococcus aureus]
>gi|5360824|dbj|BAA82194.1| site-specific recombinase [Staphylococcus aureus]
>gi|5360818|dbj|BAA82188.1| KDP operon transcriptional regulatory protein KdpE [Staphylococcus aureus]
>gi|5360811|dbj|BAA82181.1| potassium-transporting ATPase(B chanin) [Staphylococcus aureus]
>gi|5360804|dbj|BAA82174.1| ORF N003 [Staphylococcus aureus]
>gi|5360802|dbj|BAA82172.1| ORF N002 [Staphylococcus aureus]
>gi|5360800|dbj|BAA82170.1| ORF N001 [Staphylococcus aureus]
>gi|551990|gb|AAA63529.1| dihydrolipoamide dehydrogenase E2 subunit [Staphylococcus aureus]
>gi|152996|gb|AAA63531.1| dihydrolipoamide acetyltransferase E3 subunit [Staphylococcus aureus]
>gi|152995|gb|AAA63530.1| dihydrolipoamide acetyltransferase E2 subunit [Staphylococcus aureus]
>gi|577647|dbj|BAA07714.1| gamma-hemolysin [Staphylococcus aureus]
>gi|7548684|gb|AAF23273.2|AF101263_3 ABC transporter MreB [Staphylococcus aureus]
>gi|6682106|gb|AAF23274.1|AF101263_4 zinc uptake regulation protein homolog Zur [Staphylococcus aureus]
>gi|6682104|gb|AAF23272.1|AF101263_2 ABC transporter MreA [Staphylococcus aureus]
>gi|6682103|gb|AAF23271.1|AF101263_1 probable endonuclease IV [Staphylococcus aureus]
>gi|4325247|gb|AAD17309.1| superoxide dismutase SodA [Staphylococcus aureus]
>gi|7532837|gb|AAF63254.1|AF203377_2 replication initiation protein [Staphylococcus aureus]
>gi|7532836|gb|AAF63253.1|AF203377_1 replication-associated protein [Staphylococcus aureus]
>gi|7532834|gb|AAF63252.1|AF203376_2 replication initiation protein [Staphylococcus aureus]
>gi|7532833|gb|AAF63251.1|AF203376_1 replication-associated protein [Staphylococcus aureus]
>gi|7328260|emb|CAA73981.1| hypothetical protein [Staphylococcus aureus]
>gi|7328259|emb|CAA73980.1| hypothetical protein [Staphylococcus aureus]
>gi|7328258|emb|CAA73979.1| protein kinase [Staphylococcus aureus]
>gi|7328257|emb|CAA73978.1| hypothetical protein [Staphylococcus aureus]
>gi|510692|gb|AAA19777.1| enterotoxin H [Staphylococcus aureus]
>gi|7522176|pir|JC7119 Drp35 protein - Staphylococcus aureus
>gi|7470968|pir|S68971 hypothetical protein - Staphylococcus aureus
>gi|7470967|pir|JC5470 hypothetical 29.1K protein - Staphylococcus aureus
>gi|7470966|pir|T28680 fibrinogen-binding protein homolog - Staphylococcus aureus
>gi|7470965|pir|T28679 fibrinogen-binding protein homolog - Staphylococcus aureus
>gi|7470964|pir|T10908 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Staphylococcus aureus (fragment)
>gi|7470963|pir|S68731 bleomycin-binding protein - Staphylococcus aureus (fragment)
>gi|7451888|pir|S68970 triacylglycerol lipase (EC 3.1.1.3) precursor - Staphylococcus aureus
>gi|7451316|pir|JC5468 leukocidin chain lukM precursor - Staphylococcus aureus
>gi|7451314|pir|JC5469 Panton-Valentine leukocidin LukF-PV chain precursor - Staphylococcus aureus
>gi|7447124|pir|T10903 acetyltransferase (EC 2.3.1.-) vatB - Staphylococcus aureus
>gi|7443657|pir|JC5607 replication initiation protein dnaA - Staphylococcus aureus
>gi|2145582|pir|S68609 recombinase Sin - Staphylococcus aureus plasmid pSK1
>gi|2145581|pir|S66426 plasmin-sensitive surface protein - Staphylococcus aureus (fragments)
>gi|2126585|pir|PN0638 vgh protein - Staphylococcus aureus
>gi|2126584|pir|JC4555 serine-type D-Ala-D-Ala carboxypeptidase (EC 3.4.16.4) - Staphylococcus aureus
>gi|2126583|pir|JC4511 pyroglutamyl-peptidase I (EC 3.4.19.3) - Staphylococcus aureus
>gi|2126582|pir|S59955 hypothetical protein 202 - Staphylococcus aureus
>gi|2126581|pir|A55598 hypothetical protein 1 - Staphylococcus aureus (fragment)
>gi|2126580|pir|A53381 hypothetical protein (femC region) - Staphylococcus aureus (fragment)
>gi|2126579|pir|PC4078 hlgC-like protein precursor - Staphylococcus aureus
>gi|2126575|pir|S69209 alpha-toxin precursor - Staphylococcus aureus
>gi|2126574|pir|PQ0040 agrD protein - Staphylococcus aureus
>gi|2126573|pir|S58480 agrC protein - Staphylococcus aureus
>gi|2126572|pir|JC4554 ABC-type transporter homolog - Staphylococcus aureus
>gi|2119993|pir|C40585 recF protein - Staphylococcus aureus
>gi|1363415|pir|S58483 hypothetical protein 8 - Staphylococcus aureus (fragment)
>gi|1363412|pir|JC4282 gamma-hemolysin II precursor - Staphylococcus aureus
>gi|1363410|pir|S49412 fibrinogen-binding protein precursor - Staphylococcus aureus
>gi|1363398|pir|S55767 replication initiator repU - Staphylococcus aureus plasmid pUB110 (fragment)
>gi|1361357|pir|S57202 vitronectin-binding surface protein - Staphylococcus aureus (fragment)
>gi|1361356|pir|B56976 transfer protein complex trsJ - Staphylococcus aureus
>gi|1361355|pir|F56976 transfer complex protein TrsO' - Staphylococcus aureus
>gi|1361354|pir|A36891 transfer complex protein TrsN - Staphylococcus aureus plasmid pGO1
>gi|1361353|pir|E56976 transfer complex protein TrsM - Staphylococcus aureus
>gi|1361352|pir|D56976 transfer complex protein trsL - Staphylococcus aureus
>gi|1361351|pir|C56976 transfer complex protein TrsK - Staphylococcus aureus
>gi|1361349|pir|I36891 transfer complex protein TrsH - Staphylococcus aureus

>gi|1361348|pir||H36891 transfer complex protein TrsG - Staphylococcus aureus
 >gi|1361347|pir||G36891 transfer complex protein TrsF - Staphylococcus aureus
 >gi|1361346|pir||F36891 transfer complex protein TrsE - Staphylococcus aureus
 >gi|1361345|pir||E36891 transfer complex protein TrsD - Staphylococcus aureus
 >gi|1361344|pir||D36891 transfer complex protein TrsC - Staphylococcus aureus
 >gi|1361343|pir||C36891 transfer complex protein TrsB - Staphylococcus aureus
 >gi|1361342|pir||B36891 transfer complex protein TrsA - Staphylococcus aureus
 >gi|1361341|pir||S58708 neutral phosphatase - Staphylococcus aureus (ATCC 25923) (fragment)
 >gi|1361340|pir||A55856 l1m protein - Staphylococcus aureus
 >gi|1085937|pir||S42241 hypothetical protein 5 - Staphylococcus aureus plasmid pNS1
 >gi|1085933|pir||S42240 hypothetical protein 4 - Staphylococcus aureus plasmid pNS1
 >gi|1085928|pir||S42239 hypothetical protein 3 - Staphylococcus aureus plasmid pNS1
 >gi|1085919|pir||S42237 hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
 >gi|1084189|pir||S54709 hypothetical protein 81 - Staphylococcus aureus
 >gi|1075673|pir||S49271 hlgA-like protein precursor - Staphylococcus aureus
 >gi|1075672|pir||S52267 DNA polymerase III - Staphylococcus aureus
 >gi|1075671|pir||B55548 crtN protein - Staphylococcus aureus
 >gi|1075670|pir||A55548 crtM protein - Staphylococcus aureus
 >gi|1075668|pir||JC2527 alkaline shock protein - Staphylococcus aureus
 >gi|628922|pir||S43693 penicillin-binding protein 2 - Staphylococcus aureus
 >gi|543692|pir||S42238 tetracyclin resistance protein - Staphylococcus aureus plasmid pNS1
 >gi|541341|pir||S42926 hypothetical membrane spanning protein - Staphylococcus aureus
 >gi|541340|pir||S42925 probable transport protein - Staphylococcus aureus
 >gi|541339|pir||S39922 pcrB protein - Staphylococcus aureus
 >gi|541336|pir||S41539 fibrinogen-binding protein - Staphylococcus aureus
 >gi|541335|pir||A48620 adhesin - Staphylococcus aureus (fragment)
 >gi|538880|pir||B24362 chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus
 plasmid pUB112
 >gi|484391|pir||JN0627 leukocidin chain F precursor - Staphylococcus aureus
 >gi|484390|pir||JN0626 leukocidin chain S precursor - Staphylococcus aureus
 >gi|484389|pir||JN0625 gamma-hemolysin chain II precursor - Staphylococcus aureus
 >gi|482713|pir||A61069 replication protein REP - Staphylococcus aureus plasmid pOX1000
 >gi|482669|pir||A60998 replication protein REP - Staphylococcus aureus plasmid pOX2000
 >gi|481955|pir||S40262 hypothetical protein C - Staphylococcus aureus
 >gi|481954|pir||S40261 hypothetical protein B - Staphylococcus aureus
 >gi|479952|pir||S35697 leukocidin chain F - Staphylococcus aureus
 >gi|478296|pir||JN0822 acetyltransferase (EC 2.3.1.-) - Staphylococcus aureus
 >gi|478043|pir||C49238 gamma-hemolysin component, HlgC - Staphylococcus aureus
 >gi|477912|pir||B49238 gamma-hemolysin gamma 2 component, HlgB - Staphylococcus aureus
 >gi|477911|pir||B49234 leucocidin R, component F - Staphylococcus aureus
 >gi|477585|pir||A49234 leucocidin R S component - Staphylococcus aureus
 >gi|421397|pir||S11782 regulatory protein blaI - Staphylococcus aureus plasmids
 >gi|421395|pir||S11780 probable transposase - Staphylococcus aureus transposon Tn552
 >gi|421394|pir||S11781 DNA-invertase - Staphylococcus aureus transposon Tn552
 >gi|421393|pir||S11779 probable ATP-binding protein - Staphylococcus aureus transposon Tn552
 >gi|421390|pir||JN0601 heat shock protein 60 - Staphylococcus aureus
 >gi|421389|pir||JN0600 heat shock protein 10 - Staphylococcus aureus
 >gi|421388|pir||S32419 gamma-hemolysin chain H gamma II - Staphylococcus aureus
 >gi|421387|pir||S34270 fibrinogen-binding protein - Staphylococcus aureus
 >gi|421386|pir||S34269 fibrinogen-binding protein - Staphylococcus aureus
 >gi|421383|pir||S34444 blaZ protein - Staphylococcus aureus plasmid pI258 (fragment)
 >gi|421379|pir||S34447 binR protein - Staphylococcus aureus plasmid pI258 (fragment)
 >gi|322083|pir||S32211 leucocidin chain S - Staphylococcus aureus
 >gi|322082|pir||S32212 leucocidin chain F - Staphylococcus aureus
 >gi|320485|pir||A60633 tetracycline resistance protein - Staphylococcus aureus (strain MRSA101)
 >gi|320484|pir||A37389 repN protein - Staphylococcus aureus plasmid pCW7
 >gi|320483|pir||C60634 probable transposase - Staphylococcus aureus insertion sequence IS257-3
 >gi|320482|pir||B60634 probable transposase - Staphylococcus aureus insertion sequence IS257-2
 >gi|320481|pir||A60634 probable transposase - Staphylococcus aureus insertion sequence IS257-1
 >gi|320480|pir||A60757 enterotoxin C-1 - Staphylococcus aureus (fragments)
 >gi|282254|pir||A41903 recombinase homolog - Staphylococcus aureus (fragment)
 >gi|282253|pir||F42721 recombination protein recA - Staphylococcus aureus (fragment)
 >gi|282251|pir||S28101 hypothetical protein 2 - Staphylococcus aureus plasmid pC223
 >gi|282250|pir||S28102 rlx protein - Staphylococcus aureus plasmid pC223
 >gi|282249|pir||S26352 hypothetical protein - Staphylococcus aureus transposon Tn4001
 >gi|282243|pir||A42404 collagen adhesin - Staphylococcus aureus
 >gi|282241|pir||E41903 recombinase Bin3 - Staphylococcus aureus (fragment)
 >gi|282237|pir||S26353 aminoglycoside resistance protein aacA-aphD - Staphylococcus aureus
 transposon Tn4001
 >gi|282236|pir||A43848 cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus
 (fragment)

>gi|282223|pir|B43848 cell surface adhesin for heparan sulfate, 60K - *Staphylococcus aureus* (fragment)

>gi|280218|pir|A60450 hypothetical protein att155 - *Staphylococcus aureus* (fragment)

>gi|280217|pir|A44506 lactose operon repressor lacR - *Staphylococcus aureus*

>gi|97855|pir|JC1204 vga protein - *Staphylococcus aureus*

>gi|97854|pir|S12706 type II site-specific deoxyribonuclease (EC 3.1.21.4) Sau96I - *Staphylococcus aureus*

>gi|97850|pir|A41511 staphylocoagulase precursor - *Staphylococcus aureus* (strain BB)

>gi|97847|pir|JQ0759 restriction endonuclease (EC 3.1.-.-) - *Staphylococcus aureus*

>gi|97846|pir|S09566 repB protein - *Staphylococcus aureus* plasmid pBD64

>gi|97844|pir|B36242 quinolone resistance protein norA8736 - *Staphylococcus aureus* plasmid pMR8736 (fragment)

>gi|97843|pir|S12394 probable transport protein qacA - *Staphylococcus aureus* plasmid pSK1

>gi|97838|pir|S12093 probable transposase - *Staphylococcus aureus* insertion sequence IS431mec

>gi|97836|pir|A36242 norA209 protein - *Staphylococcus aureus* plasmid pSA209 (fragment)

>gi|97835|pir|A37838 norA protein - *Staphylococcus aureus*

>gi|97834|pir|S09565 neomycin resistance protein - *Staphylococcus aureus* plasmid pBD64

>gi|97831|pir|JQ0773 penicillin-binding protein mecA, low-affinity - *Staphylococcus aureus*

>gi|97830|pir|S19207 leucocidin R component F precursor - *Staphylococcus aureus*

>gi|97829|pir|A30471 hypothetical protein rep - *Staphylococcus aureus* plasmid pSK89

>gi|97828|pir|B30471 hypothetical protein cop - *Staphylococcus aureus* plasmid pSK89

>gi|97824|pir|S20793 hypothetical protein 5 - *Staphylococcus aureus*

>gi|97820|pir|S12393 hypothetical protein (qacA 5' region) - *Staphylococcus aureus* plasmid pSK1

>gi|97819|pir|S14179 hypothetical protein 140 - *Staphylococcus aureus*

>gi|97815|pir|B38158 galactose-6-phosphate isomerase 19K chain - *Staphylococcus aureus*

>gi|97814|pir|A38158 galactose-6-phosphate isomerase (EC 5.1.3.-) 15K chain - *Staphylococcus aureus*

>gi|97813|pir|S19702 fibronectin-binding protein B - *Staphylococcus aureus*

>gi|97812|pir|A32192 fibronectin-binding protein - *Staphylococcus aureus*

>gi|97804|pir|S16509 DNA-invertase - *Staphylococcus aureus* transposon Tn552

>gi|97795|pir|S09246 coagulase precursor - *Staphylococcus aureus* (strain 8325-4)

>gi|97793|pir|C34643 cathepsin E (EC 3.4.23.34) - *Staphylococcus aureus* (fragments)

>gi|97788|pir|S09385 DNA-invertase homolog bin3 - *Staphylococcus aureus* transposon Tn555

>gi|97786|pir|S15324 beta-hemolysin - *Staphylococcus aureus*

>gi|97783|pir|B41589 40K elastin-binding protein - *Staphylococcus aureus* (fragment)

>gi|97782|pir|A41589 25K elastin-binding protein - *Staphylococcus aureus* (fragment)

>gi|80324|pir|A24456 kanamycin nucleotidyltransferase (EC 2.7.7.-) - *Staphylococcus aureus* plasmid pUB110

>gi|79917|pir|S06782 tryptophan synthase (EC 4.2.1.20) - *Staphylococcus aureus* (fragment)

>gi|79916|pir|A24545 triacylglycerol lipase (EC 3.1.1.3) - *Staphylococcus aureus*

>gi|79915|pir|C24584 transposition regulatory protein tnpC - *Staphylococcus aureus* transposon Tn554

>gi|79914|pir|B24584 transposition regulatory protein tnpB - *Staphylococcus aureus* transposon Tn554

>gi|79913|pir|A24584 transposition regulatory protein tnpA - *Staphylococcus aureus* transposon Tn554

>gi|79912|pir|S04166 transposase 2 - *Staphylococcus aureus* transposon Tn4003

>gi|79911|pir|S04162 transposase 1 - *Staphylococcus aureus* transposon Tn4003

>gi|79910|pir|JS0296 transposase - *Staphylococcus aureus*

>gi|79906|pir|S06744 staphylocoagulase precursor - *Staphylococcus aureus*

>gi|79905|pir|A25620 staphylocoagulase - *Staphylococcus aureus* (fragment)

>gi|79903|pir|S00935 rlx protein - *Staphylococcus aureus* plasmid pS194

>gi|79902|pir|A29827 replication protein REP - *Staphylococcus aureus* plasmids

>gi|79901|pir|S00909 replication initiation protein - *Staphylococcus aureus* plasmid pc223

>gi|79900|pir|A30480 repJ protein - *Staphylococcus aureus* plasmid pc223

>gi|79899|pir|JT0372 repI protein - *Staphylococcus aureus* plasmid pUB112

>gi|79898|pir|S00937 repE protein - *Staphylococcus aureus* plasmid pS194

>gi|79896|pir|A29605 protein A precursor - *Staphylococcus aureus* (strain Cowan 1)

>gi|79894|pir|S20576 probable regulatory protein mecI - *Staphylococcus aureus*

>gi|79891|pir|B28474 phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor II - *Staphylococcus aureus*

>gi|79887|pir|JQ1147 N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) - *Staphylococcus aureus*

>gi|79886|pir|JQ1439 multidrug resistance protein - *Staphylococcus aureus* plasmids

>gi|79884|pir|G29504 hypothetical 20K protein (mer regulatory region) - *Staphylococcus aureus* plasmid pI258

>gi|79883|pir|C29504 hypothetical 24K protein (mer operon) - *Staphylococcus aureus* plasmid pI258

>gi|79882|pir|B29504 hypothetical 18K protein (mer operon) - *Staphylococcus aureus* plasmid pI258

>gi|79881|pir|A29504 hypothetical 16K protein (mer operon) - *Staphylococcus aureus* plasmid pI258

>gi|79880|pir|D29504 hypothetical 14K protein (mer operon) - *Staphylococcus aureus* plasmid pI258

>gi|79879|pir|S20575 mecRI protein - *Staphylococcus aureus*

>gi|79877|pir|A31901 lincomycin resistance protein linA' - *Staphylococcus aureus* (strain BM4611)

>gi|79875|pir|JQ1530 leukocidin chain F precursor - *Staphylococcus aureus*

>gi|79874|pir|S04359 lacD protein - *Staphylococcus aureus*

>gi|79871|pir|S00936 hypothetical protein D - *Staphylococcus aureus* plasmid pS194

>gi|79869|pir|S15767 hypothetical protein 2 (h1b 3' region) - *Staphylococcus aureus* (fragment)

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>gi|79868|pir||S15765 hypothetical protein 1 (hnb 5' region) - Staphylococcus aureus (fragment)
>gi|79867|pir||F24584 hypothetical protein - Staphylococcus aureus transposon Tn554
>gi|79866|pir||S04165 hypothetical protein - Staphylococcus aureus plasmid pSK1 transposon Tn4003
>gi|79865|pir||S06784 hypothetical protein (femA 3' region) - Staphylococcus aureus
>gi|79864|pir||B32561 cadC protein - Staphylococcus aureus plasmid pI258
>gi|79863|pir||A41652 probable glycerophosphodiester phosphodiesterase (EC 3.1.4.46) -
Staphylococcus aureus
>gi|79862|pir||S06783 femA protein - Staphylococcus aureus
>gi|79857|pir||JG0016 epidermal cell differentiation inhibitor precursor - Staphylococcus aureus
>gi|79843|pir||JQ0387 agrB protein - Staphylococcus aureus
>gi|79842|pir||A32357 accessory gene regulatory protein agrA - Staphylococcus aureus
>gi|7437965|pir||JC6560 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) -
Staphylococcus aureus
>gi|7434769|pir||S34442 transcription initiation factor sigma plaC - Staphylococcus aureus
>gi|2144945|pir||QVSAA protein A precursor - Staphylococcus aureus
>gi|2144683|pir||ENSAC1 enterotoxin C-1 precursor - Staphylococcus aureus
>gi|2144682|pir||ENSAB6 enterotoxin B precursor - Staphylococcus aureus
>gi|2126578|pir||S54426 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Staphylococcus
aureus
>gi|2126577|pir||S54427 gyrase-like protein alpha chain - Staphylococcus aureus
>gi|2126576|pir||S59956 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Staphylococcus aureus
(fragment)
>gi|2119116|pir||S59954 ribosomal protein L7/L12 - Staphylococcus aureus (fragment)
>gi|2117996|pir||A53641 arsenate reductase (EC 1.-.-.-) - Staphylococcus aureus plasmid pI258
>gi|2117910|pir||S59951 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Staphylococcus aureus
>gi|1363411|pir||S58814 cell division protein ftsZ - Staphylococcus aureus
>gi|1361350|pir||A56976 transfer complex protein TrsI - Staphylococcus aureus
>gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus
aureus
>gi|1075676|pir||S54793 superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - Staphylococcus aureus
(fragment)
>gi|1075669|pir||S52934 alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - Staphylococcus
aureus (fragment)
>gi|625852|pir||JP0045 ribosomal protein L30 - Staphylococcus aureus (fragment)
>gi|541338|pir||S39923 DNA helicase pcrA - Staphylococcus aureus
>gi|541337|pir||S40178 isoleucine--tRNA ligase (EC 6.1.1.5) - Staphylococcus aureus
>gi|538884|pir||B46568 ermC protein - Staphylococcus aureus plasmid pT48
>gi|538882|pir||A40585 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Staphylococcus
aureus
>gi|538881|pir||B40585 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain A - Staphylococcus
aureus
>gi|538608|pir||A24362 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus
plasmid pUB112
>gi|482777|pir||A61152 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus
plasmid pSCS7
>gi|421382|pir||S11783 bla regulator protein blaR1 - Staphylococcus aureus plasmids
>gi|322081|pir||S32014 dihydrofolate reductase (EC 1.5.1.3) - Staphylococcus aureus
>gi|322080|pir||A44849 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus
plasmid
>gi|282240|pir||B41903 arsenical resistance operon repressor - Staphylococcus aureus plasmid pI258
>gi|282239|pir||D41903 arsenate reductase (EC 1.-.-.-) - Staphylococcus aureus plasmid pI258
>gi|282238|pir||C41903 arsenical pump membrane protein - Staphylococcus aureus
>gi|279459|pir||YXSAT3 thymidylate synthase (EC 2.1.1.45) - Staphylococcus aureus plasmid pSK1
transposon Tn4003
>gi|98263|pir||A36141 cop protein - Staphylococcus aureus plasmid pE194
>gi|97849|pir||S12705 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) Sau96I -
Staphylococcus aureus
>gi|97842|pir||S19721 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) chain E1-beta - Staphylococcus
aureus (fragment)
>gi|97837|pir||A31048 phosphotransferase system enzyme II (EC 2.7.1.69), mannitol-specific, factor
III - Staphylococcus aureus (fragments)
>gi|97833|pir||JQ0760 methyltransferase (EC 2.1.1.-) - Staphylococcus aureus
>gi|97832|pir||S20433 lipoprotein signal peptidase (EC 3.4.23.36) - Staphylococcus aureus
>gi|97826|pir||S20799 hypothetical protein 7 - Staphylococcus aureus
>gi|97816|pir||S21758 glutamic acid-specific endopeptidase - Staphylococcus aureus
>gi|97807|pir||A33953 enterotoxin D precursor - Staphylococcus aureus
>gi|97805|pir||S11885 enterotoxin C3 - Staphylococcus aureus
>gi|97798|pir||S19723 dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Staphylococcus aureus
>gi|97797|pir||S19722 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) chain E2 - Staphylococcus
aureus
>gi|97787|pir||A35001 beta-lactamase (EC 3.5.2.6) PSE-4 precursor - Staphylococcus aureus
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>gi|80332|pir||B29827 macrolide/lincosamide/streptogramin B resistance methylase - *Staphylococcus aureus* plasmid pE5
>gi|79907|pir||S00938 str protein - *Staphylococcus aureus* plasmid pS194
>gi|79904|pir||D24584 spectinomycin resistance protein spc - *Staphylococcus aureus* transposon Tn554
>gi|79893|pir||A32561 probable cadmium-transporting ATPase (EC 3.6.1.-) - *Staphylococcus aureus*
>gi|79888|pir||F29504 alkylmercury lyase (EC 4.99.1.2) - *Staphylococcus aureus* plasmid pI258
>gi|79885|pir||E29504 mercury(II) reductase (EC 1.16.1.1) - *Staphylococcus aureus* plasmid pI258
>gi|79878|pir||A25101 erythromycin resistance protein ermA - *Staphylococcus aureus* transposon Tn554
>gi|79873|pir||S04358 lacC protein - *Staphylococcus aureus*
>gi|79861|pir||A26050 exfoliative toxin B precursor - *Staphylococcus aureus*
>gi|79856|pir||A28179 enterotoxin E precursor - *Staphylococcus aureus*
>gi|79855|pir||A60114 enterotoxin C-2 precursor - *Staphylococcus aureus*
>gi|79853|pir||A28664 enterotoxin A precursor - *Staphylococcus aureus*
>gi|79851|pir||S04164 dihydrofolate reductase (EC 1.5.1.3) - *Staphylococcus aureus* plasmid pSK1
transposon Tn4003
>gi|79844|pir||A27233 beta-galactosidase (EC 3.2.1.23) - *Staphylococcus aureus*
>gi|76321|pir||QOSAC2 hypothetical protein C - *Staphylococcus aureus* plasmid pC221
>gi|76320|pir||QOSAA2 rlx protein - *Staphylococcus aureus* plasmid pC221
>gi|76319|pir||QOSA8T hypothetical protein B-189 - *Staphylococcus aureus* plasmid pT181
>gi|76318|pir||QOSAEC hypothetical protein E-229 - *Staphylococcus aureus* plasmid pC194
>gi|76317|pir||QOSACC hypothetical protein C-120 - *Staphylococcus aureus* plasmid pC194
>gi|76316|pir||QOSA7C hypothetical protein E-74 - *Staphylococcus aureus* plasmid pC194
>gi|76315|pir||QOSACE hypothetical protein C-102 - *Staphylococcus aureus* plasmid pE194
>gi|76314|pir||QOSABE hypothetical protein B-111 - *Staphylococcus aureus* plasmid pE194
>gi|73155|pir||RQSAD2 repD protein - *Staphylococcus aureus* plasmid pC221
>gi|73154|pir||RQSACT repC protein - *Staphylococcus aureus* plasmids
>gi|73152|pir||LFSAP9 ermC leader peptide - *Staphylococcus aureus* plasmids
>gi|72984|pir||QOSA4E hypothetical protein C-403 - *Staphylococcus aureus* plasmid pE194
>gi|72843|pir||QOSACT hypothetical protein C-156 - *Staphylococcus aureus* plasmid pT181
>gi|72842|pir||QOSABT hypothetical protein B-295 - *Staphylococcus aureus* plasmid pT181
>gi|72420|pir||WPSAHP phosphotransferase system phosphohistidine-containing protein - *Staphylococcus aureus*
>gi|69625|pir||XCSAS1 toxic shock syndrome toxin-1 precursor - *Staphylococcus aureus*
>gi|69556|pir||LESAD delta hemolysin - *Staphylococcus aureus*
>gi|67766|pir||PNSAP beta-lactamase (EC 3.5.2.6) precursor - *Staphylococcus aureus*
>gi|67543|pir||PRSAEB epidermolytic toxin B precursor - *Staphylococcus aureus* plasmid pRW001
>gi|67542|pir||PRSAEA epidermolytic toxin A precursor - *Staphylococcus aureus*
>gi|67541|pir||PRSASK glutamyl endopeptidase (EC 3.4.21.19) precursor - *Staphylococcus aureus*
>gi|67305|pir||NCSAF micrococcal nuclease (EC 3.1.31.1) precursor - *Staphylococcus aureus*
>gi|66882|pir||PKSAF kanamycin kinase (EC 2.7.1.95) - *Staphylococcus aureus*
>gi|66872|pir||WQSA3L phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor III - *Staphylococcus aureus*
>gi|66524|pir||XXSAC2 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - *Staphylococcus aureus* plasmid pC221
>gi|66523|pir||XXSACC chloramphenicol O-acetyltransferase (EC 2.3.1.28) - *Staphylococcus aureus* plasmids
>gi|66452|pir||YESA9E rRNA (adenine-N6-)-methyltransferase (EC 2.1.1.48) - *Staphylococcus aureus* plasmids
>gi|7381167|gb|AAF61418.1|AF135268_1 ribonuclease P protein component [*Staphylococcus aureus*]
>gi|6648971|gb|AAF21314.1| site-specific recombinase [*Staphylococcus aureus*]
>gi|6648970|gb|AAF21313.1|AF118839_1 iron uptake regulatory protein; Fur [*Staphylococcus aureus*]
>gi|7330783|gb|AAF60251.1| Geh [*Staphylococcus aureus*]
>gi|7330782|gb|AAF60250.1| IcaC [*Staphylococcus aureus*]
>gi|7330780|gb|AAF60249.1| Geh [*Staphylococcus aureus*]
>gi|7330779|gb|AAF60248.1| IcaC [*Staphylococcus aureus*]
>gi|7330777|gb|AAF60247.1| Geh [*Staphylococcus aureus*]
>gi|7330776|gb|AAF60246.1| IcaC [*Staphylococcus aureus*]
>gi|7330774|gb|AAF60245.1| Geh [*Staphylococcus aureus*]
>gi|7330773|gb|AAF60244.1| IcaC [*Staphylococcus aureus*]
>gi|7330771|gb|AAF60243.1| Geh [*Staphylococcus aureus*]
>gi|7330770|gb|AAF60242.1| IcaC [*Staphylococcus aureus*]
>gi|7330768|gb|AAF60241.1| HprK [*Staphylococcus aureus*]
>gi|7330767|gb|AAF60240.1| UvrA [*Staphylococcus aureus*]
>gi|7330765|gb|AAF60239.1| HprK [*Staphylococcus aureus*]
>gi|7330764|gb|AAF60238.1| UvrA [*Staphylococcus aureus*]
>gi|7330762|gb|AAF60237.1| HprK [*Staphylococcus aureus*]
>gi|7330761|gb|AAF60236.1| UvrA [*Staphylococcus aureus*]
>gi|7330759|gb|AAF60235.1| HprK [*Staphylococcus aureus*]
>gi|7330758|gb|AAF60234.1| UvrA [*Staphylococcus aureus*]
>gi|7330756|gb|AAF60233.1| HprK [*Staphylococcus aureus*]
>gi|7330755|gb|AAF60232.1| UvrA [*Staphylococcus aureus*]

>gi|7330753|gb|AAF60231.1| HprK [Staphylococcus aureus]
 >gi|7330752|gb|AAF60230.1| UvrA [Staphylococcus aureus]
 >gi|6671351|gb|AAF23170.1|AF210055_3 AgrC [Staphylococcus aureus]
 >gi|6671350|gb|AAF23169.1|AF210055_2 AgrD [Staphylococcus aureus]
 >gi|6671349|gb|AAF23168.1|AF210055_1 AgrB [Staphylococcus aureus]
 >gi|7328298|emb|CAB82464.1| transketolase, putative [Staphylococcus aureus]
 >gi|7328297|emb|CAB82463.1| SOS regulatory LexA protein, putative [Staphylococcus aureus]
 >gi|7328295|emb|CAB82462.1| DNA mismatch repair protein [Staphylococcus aureus]
 >gi|7328294|emb|CAB82461.1| DNA mismatch repair protein [Staphylococcus aureus]
 >gi|7328292|emb|CAB82460.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328291|emb|CAB82459.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328290|emb|CAB82458.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328289|emb|CAB82457.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328288|emb|CAB82456.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328284|emb|CAB82466.1| MutS protein [Staphylococcus aureus]
 >gi|7328280|emb|CAB82478.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328279|emb|CAB82477.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328278|emb|CAB82476.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328277|emb|CAB82475.1| D-alanine aminotransferase [Staphylococcus aureus]
 >gi|7328276|emb|CAB82474.1| putative peptidase [Staphylococcus aureus]
 >gi|7328275|emb|CAB82473.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328274|emb|CAB82472.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328272|emb|CAB82471.1| ORF314 [Staphylococcus aureus]
 >gi|7328271|emb|CAB82470.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328270|emb|CAB82469.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328269|emb|CAB82468.1| hypothetical protein [Staphylococcus aureus]
 >gi|7106006|emb|CAB75986.1| ornithine carbamoyltransferase [Staphylococcus aureus]
 >gi|7272362|gb|AAA26601.2| blaZ [Staphylococcus aureus]
 >gi|152968|gb|AAA26604.1| binR [Staphylococcus aureus]
 >gi|152967|gb|AAA26603.1| blaI [Staphylococcus aureus]
 >gi|152966|gb|AAA26602.1| blaR1 [Staphylococcus aureus]
 >gi|7242216|gb|AAB32123.2| porphobilinogen synthase; PBG; HemB [Staphylococcus aureus]
 >gi|7239722|gb|AAA71951.2| putative [Staphylococcus aureus]
 >gi|7239370|gb|AAF43206.1|AF230358_3 accessory gene regulator protein D [Staphylococcus aureus]
 >gi|7239369|gb|AAF43205.1|AF230358_2 accessory gene regulator protein B [Staphylococcus aureus]
 >gi|7239368|gb|AAF43204.1|AF230358_1 delta-haemolysin precursor [Staphylococcus aureus]
 >gi|310620|gb|AAA71964.1| putative [Staphylococcus aureus]
 >gi|310619|gb|AAA71963.1| putative [Staphylococcus aureus]
 >gi|310618|gb|AAA71962.1| putative [Staphylococcus aureus]
 >gi|310617|gb|AAA71961.1| putative [Staphylococcus aureus]
 >gi|310616|gb|AAA71960.1| putative [Staphylococcus aureus]
 >gi|310615|gb|AAA71959.1| putative [Staphylococcus aureus]
 >gi|310614|gb|AAA71958.1| putative [Staphylococcus aureus]
 >gi|310613|gb|AAA71957.1| putative [Staphylococcus aureus]
 >gi|310612|gb|AAA71956.1| putative [Staphylococcus aureus]
 >gi|310611|gb|AAA71955.1| putative [Staphylococcus aureus]
 >gi|310610|gb|AAA71954.1| putative [Staphylococcus aureus]
 >gi|310609|gb|AAA71953.1| putative [Staphylococcus aureus]
 >gi|310608|gb|AAA71952.1| putative [Staphylococcus aureus]
 >gi|4126683|dbj|BAA36693.1| enterotoxin type Gv [Staphylococcus aureus]
 >gi|7162103|emb|CAB76672.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162101|emb|CAB76671.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162099|emb|CAB76670.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162097|emb|CAB76669.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162095|emb|CAB76668.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162093|emb|CAB76667.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162091|emb|CAB76666.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162089|emb|CAB76665.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162087|emb|CAB76664.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162085|emb|CAB76663.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162083|emb|CAB76662.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162081|emb|CAB76661.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162079|emb|CAB76660.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162077|emb|CAB76659.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162075|emb|CAB76658.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162073|emb|CAB76657.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162071|emb|CAB76656.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162069|emb|CAB76655.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162067|emb|CAB76654.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162065|emb|CAB76653.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162063|emb|CAB76652.1| triosephosphate isomerase [Staphylococcus aureus]

[illegible]

>gi|7161911|emb|CAB76580.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161909|emb|CAB76579.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161907|emb|CAB76578.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161905|emb|CAB76577.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161903|emb|CAB76576.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161901|emb|CAB76575.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161899|emb|CAB76574.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161897|emb|CAB76573.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161887|emb|CAB76839.1| Catalase [Staphylococcus aureus]
>gi|7161885|emb|CAB76840.1| Catalase [Staphylococcus aureus]
>gi|7107452|gb|AAF36410.1|AF235026_1 pyruvate dehydrogenase beta subunit PdhB [Staphylococcus aureus]
>gi|7106008|emb|CAB75987.1| ornithine carbamoyltransferase Otc6850 [Staphylococcus aureus]
>gi|7106004|emb|CAB75985.1| extracellular matrix and plasma binding protein [Staphylococcus aureus]
>gi|7106002|emb|CAB75984.1| extracellular matrix and plasma binding protein [Staphylococcus aureus]
>gi|7019229|emb|CAB75732.1| bone sialoprotein-binding protein [Staphylococcus aureus]
>gi|6180191|gb|AAF05840.1|AF197058_1 trans-2-enoyl-ACP reductase [Staphylococcus aureus]
>gi|6967305|emb|CAB72943.1| hypothetical protein [Staphylococcus aureus]
>gi|6967304|emb|CAB72942.1| hypothetical protein [Staphylococcus aureus]
>gi|6967303|emb|CAB72941.1| hypothetical protein [Staphylococcus aureus]
>gi|6967301|emb|CAB72940.1| hypothetical protein [Staphylococcus aureus]
>gi|6967300|emb|CAB72939.1| hypothetical protein [Staphylococcus aureus]
>gi|6912039|emb|CAB72261.1| penicillin-binding protein 3 [Staphylococcus aureus]
>gi|2506027|dbj|BAA22600.1| NAG [Staphylococcus aureus]
>gi|577649|dbj|BAA07715.1| preLUKM [Staphylococcus aureus]
>gi|216971|dbj|BAA00630.1| glutamic acid specific protease prepropeptide [Staphylococcus aureus]
>gi|6119707|emb|CAB59570.1| aureolysin [Staphylococcus aureus]
>gi|6119705|emb|CAB59569.1| aureolysin [Staphylococcus aureus]
>gi|6119703|emb|CAB59568.1| aureolysin [Staphylococcus aureus]
>gi|6119701|emb|CAB59567.1| aureolysin [Staphylococcus aureus]
>gi|6729657|emb|CAB67709.1| secretory protein [Staphylococcus aureus]
>gi|6729716|pdb|1BQB|A Chain A, Aureolysin, Staphylococcus Aureus Metalloproteinase
>gi|5107600|pdb|1KGG|A Chain A, Structure Of Beta-Lactamase Glu166gln:asn170asp Mutant
>gi|6110605|gb|AAF03894.1|AF193842_1 DNA polymerase I [Staphylococcus aureus]
>gi|6690335|gb|AAF24091.1|AF117259_3 ATP binding protein VgA [Staphylococcus aureus]
>gi|6690334|gb|AAF24090.1|AF117259_2 unknown [Staphylococcus aureus]
>gi|6690333|gb|AAF24089.1|AF117259_1 replication protein [Staphylococcus aureus]
>gi|6690331|gb|AAF24088.1|AF117258_5 hydrolase VgB [Staphylococcus aureus]
>gi|6690330|gb|AAF24087.1|AF117258_4 acetyltransferase Vat [Staphylococcus aureus]
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>gi|6690328|gb|AAF24085.1|AF117258_2 unknown [Staphylococcus aureus]
>gi|6690327|gb|AAF24084.1|AF117258_1 replication protein RepE [Staphylococcus aureus]
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>gi|6689207|emb|CAB65401.1| VicK protein [Staphylococcus aureus]
>gi|6689206|emb|CAB65400.1| TycG protein [Staphylococcus aureus]
>gi|6689205|emb|CAB65399.1| VicR protein [Staphylococcus aureus]
>gi|6681575|dbj|BAA88759.1| cassette chromosome recombinase B [Staphylococcus aureus]
>gi|6681574|dbj|BAA88758.1| cassette chromosome recombinase A [Staphylococcus aureus]
>gi|6681572|dbj|BAA88757.1| cassette chromosome recombinase B [Staphylococcus aureus]
>gi|6681571|dbj|BAA88756.1| cassette chromosome recombinase A [Staphylococcus aureus]
>gi|6681569|dbj|BAA88755.1| cassette chromosome recombinase B [Staphylococcus aureus]
>gi|6681568|dbj|BAA88754.1| cassette chromosome recombinase A [Staphylococcus aureus]
>gi|6644368|gb|AAF21032.1|AF209197_1 UDP-GlcNAc 2-epimerase [Staphylococcus aureus]
>gi|6594284|dbj|BAA88420.1| ATP-binding protein [Staphylococcus aureus]
>gi|6594283|dbj|BAA88419.1| hydrophobic transmembrane protein [Staphylococcus aureus]
>gi|6594281|dbj|BAA88418.1| MsrSA [Staphylococcus aureus]
>gi|6594280|dbj|BAA88417.1| ATP-binding protein [Staphylococcus aureus]
>gi|6594279|dbj|BAA88416.1| hydrophobic transmembrane protein [Staphylococcus aureus]
>gi|6594277|dbj|BAA88415.1| MsrSA [Staphylococcus aureus]
>gi|6594276|dbj|BAA88414.1| ATP-binding protein [Staphylococcus aureus]
>gi|6594275|dbj|BAA88413.1| hydrophobic transmembrane protein [Staphylococcus aureus]
>gi|6578925|gb|AAF18137.1|AF205033_3 glutamyl-tRNAGln amidotransferase subunit B [Staphylococcus aureus]
>gi|6578924|gb|AAF18136.1|AF205033_2 glutamyl-tRNAGln amidotransferase subunit A [Staphylococcus aureus]
>gi|6578923|gb|AAF18135.1|AF205033_1 glutamyl-tRNAGln amidotransferase subunit C [Staphylococcus aureus]
>gi|4185565|gb|AAD09131.1| surface protein Pls [Staphylococcus aureus]
>gi|6492112|gb|AAF14183.1| putative transmembrane protein [Staphylococcus aureus]

>gi|6492111|gb|AAF14182.1|AF105976_1 FemX [Staphylococcus aureus]
>gi|6441050|dbj|BAA86894.1| Drp35 [Staphylococcus aureus]
>gi|6434054|emb|CAB60756.1| permease [Staphylococcus aureus]
>gi|6434053|emb|CAB60755.1| ATP-binding protein [Staphylococcus aureus]
>gi|6434052|emb|CAB60754.1| hypothetical protein [Staphylococcus aureus]
>gi|6434050|emb|CAB60753.1| anthranilate synthase component II [Staphylococcus aureus]
>gi|6434049|emb|CAB60752.1| anthranilate phosphoribosyltransferase [Staphylococcus aureus]
>gi|6434048|emb|CAB60751.1| indole-3-glycerol phosphate synthase [Staphylococcus aureus]
>gi|6434047|emb|CAB60750.1| phosphoriborylanthranilate isomerase [Staphylococcus aureus]
>gi|6434045|emb|CAB60749.1| hypothetical protein [Staphylococcus aureus]
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>gi|6434042|emb|CAB60747.1| hypothetical protein [Staphylococcus aureus]
>gi|6434041|emb|CAB60746.1| hypothetical protein [Staphylococcus aureus]
>gi|6434040|emb|CAB60745.1| hypothetical protein [Staphylococcus aureus]
>gi|6434038|emb|CAB60744.1| hypothetical protein [Staphylococcus aureus]
>gi|6434037|emb|CAB60743.1| thioredoxine reductase [Staphylococcus aureus]
>gi|6434035|emb|CAB60742.1| hypothetical protein [Staphylococcus aureus]
>gi|6434034|emb|CAB60741.1| hypothetical protein [Staphylococcus aureus]
>gi|6434033|emb|CAB60740.1| thioredoxine reductase [Staphylococcus aureus]
>gi|6434031|emb|CAB60739.1| porphobilinogen synthase [Staphylococcus aureus]
>gi|6434030|emb|CAB60738.1| GSA-1-aminotransferase [Staphylococcus aureus]
>gi|6434029|emb|CAB60737.1| yhjN protein [Staphylococcus aureus]
>gi|6434028|emb|CAB60736.1| DNA-3-methyladenine glycosidase [Staphylococcus aureus]
>gi|6273682|emb|CAA73924.1| transposase [Staphylococcus aureus]
>gi|6273681|emb|CAA73923.1| resolvase [Staphylococcus aureus]
>gi|6273680|emb|CAA73922.1| hypothetical protein [Staphylococcus aureus]
>gi|6273679|emb|CAA73921.1| rRNA methylase [Staphylococcus aureus]
>gi|6273678|emb|CAA73925.1| hypothetical protein [Staphylococcus aureus]
>gi|6166144|sp|Q53665|DPO3_STAAU DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
>gi|3915801|sp|P50073|PARC_STAAU TOPOISOMERASE IV SUBUNIT A
>gi|2507345|sp|P47770|RPOC_STAAU DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN)
(RNA POLYMERASE BETA' SUBUNIT)
>gi|135552|sp|P02983|TCR_STAAU TETRACYCLINE RESISTANCE PROTEIN
>gi|130885|sp|P22490|PRE2_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
>gi|128852|sp|P00644|NUC_STAAU THERMONUCLEASE PRECURSOR (TNASE) (MICROCOCCAL NUCLEASE)
(STAPHYLOCOCCAL NUCLEASE)
>gi|126941|sp|P26597|MECR_STAEP METHICILLIN RESISTANCE MECR1 PROTEIN
>gi|6137706|pdb|1QTF|A Chain A, Crystall Structure Of Exfoliative Toxin B
>gi|4557981|pdb|1SBB|D Chain D, T-Cell Receptor Beta Chain Complexed With Superantigen Seb
>gi|4557979|pdb|1SBB|B Chain B, T-Cell Receptor Beta Chain Complexed With Superantigen Seb
>gi|3025223|sp|Q53719|YLY1_STAAU HYPOTHETICAL 18.6 KD PROTEIN IN LYTA 3'REGION (ORF1)
>gi|2811052|sp|O07319|YLLB_STAAU HYPOTHETICAL 17.4 KD PROTEIN
>gi|2500373|sp|Q53602|YBXF_STAAU PROBABLE RIBOSOMAL PROTEIN IN RPSL 5'REGION
>gi|2226349|gb|AAB61744.1| CspC [Staphylococcus aureus]
>gi|2226347|gb|AAB61743.1| CspB [Staphylococcus aureus]
>gi|1723202|sp|P55177|YAG5_STAAU HYPOTHETICAL 29.8 KD PROTEIN IN AGR OPERON (ORF 5)
>gi|1176334|sp|P41370|YIL2_STAAU HYPOTHETICAL PROTEIN IN ILES 3'REGION (ORF C)
>gi|1176333|sp|P41369|YIL1_STAAU HYPOTHETICAL PROTEIN IN ILES 5'REGION (ORF B)
>gi|141232|sp|P03860|YPCD_STAAU HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D)
>gi|141195|sp|P14503|YP2C_STAAU HYPOTHETICAL 27.7 KD PROTEIN
>gi|141194|sp|P12052|YP2B_STAAU HYPOTHETICAL 27.0 KD PROTEIN (ORFD)
>gi|141193|sp|P03866|YP2A_STAAU HYPOTHETICAL 26.9 KD PROTEIN (HYPOTHETICAL PROTEIN C)
>gi|141190|sp|P23217|YP23_STAAU HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN QACA 5'REGION (ORF 188)
>gi|141183|sp|P13977|YP15_STAAU HYPOTHETICAL 15.5 KD PROTEIN
>gi|141180|sp|P03859|YP12_STAAU HYPOTHETICAL 12.4 KD PROTEIN (READING FRAME C)
>gi|141043|sp|P08655|YMER_STAAU HYPOTHETICAL 19.7 KD PROTEIN IN MERCURIC RESISTANCE OPERON
>gi|140780|sp|P21224|YHLB_STAAU HYPOTHETICAL PROTEIN IN HLB 3'REGION
>gi|1718087|sp|P26839|VATA_STAAU VIRGINIAMYCIN A ACETYLTANSFERASE
>gi|138137|sp|P17978|VGB_STAAU VIRGINIAMYCIN B HYDROLASE (VGB)
>gi|136457|sp|P06886|TSST_STAAU TOXIC SHOCK SYNDROME TOXIN-1 PRECURSOR (TSST-1)
>gi|6094457|sp|Q53770|TETM_STAAU TETRACYCLINE RESISTANCE PROTEIN TETM (TETA(M))
>gi|6093662|sp|Q53596|PCP_STAAU PYRROLIDONE-CARBOXYLATE PEPTIDASE (5-OXOPROLYL-PEPTIDASE)
(PYROGLUTAMYL-PEPTIDASE I) (PGP-I) (PYRASE)
>gi|3915844|sp|Q33276|RRF_STAAU PROBABLE RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF)
>gi|3915057|sp|Q32422|SYH_STAAU HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
>gi|3914612|sp|Q50581|RECG_STAAU ATP-DEPENDENT DNA HELICASE RECG
>gi|3287914|sp|P81297|STPA_STAAU STAPHOPAIN
>gi|3122859|sp|Q08387|SECY_STAAU PREPROTEIN TRANSLOCASE SECY SUBUNIT
>gi|3122722|sp|Q06444|RL30_STAAU 50S RIBOSOMAL PROTEIN L30
>gi|3024594|sp|Q06442|SECE_STAAU PREPROTEIN TRANSLOCASE SECE SUBUNIT
>gi|3024540|sp|Q06443|RL11_STAAU 50S RIBOSOMAL PROTEIN L11

>gi|3024239|sp|008386|NUSG_STAAU TRANSCRIPTION ANTITERMINATION PROTEIN NUSG
>gi|2501053|sp|P95689|SYS_STAAU SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
>gi|2501020|sp|Q53638|SYK_STAAU LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)
>gi|2500269|sp|O06445|RL15_STAAU 50S RIBOSOMAL PROTEIN L15
>gi|1710069|sp|P29232|RECF_STAAU RECF PROTEIN
>gi|1709892|sp|P02907|PTHP_STAAU PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN)
>gi|1709733|sp|P51065|PPCK_STAAU PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
>gi|1709584|sp|P50072|PARE_STAAU TOPOISOMERASE IV SUBUNIT B
>gi|1709245|sp|P50588|NDK_STAAU NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE)
>gi|1351009|sp|P48940|RS7_STAAU 30S RIBOSOMAL PROTEIN S7
>gi|1350927|sp|P48942|RS12_STAAU 30S RIBOSOMAL PROTEIN S12
>gi|1350849|sp|P47768|RPOB_STAAU DNA-DIRECTED RNA POLYMERASE BETA CHAIN (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT)
>gi|1350771|sp|P48860|RL7_STAAU 50S RIBOSOMAL PROTEIN L7/L12
>gi|1346789|sp|P03864|PRE3_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
>gi|1346788|sp|P03857|PRE1_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
>gi|1175774|sp|P45557|PRMA_STAAU PROBABLE METHYLTRANSFERASE
>gi|1174516|sp|P41368|SYIP_STAAU ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT (ISOLEUCINE--TRNA LIGASE) (ILERS) (MUPIROCIN RESISTANCE PROTEIN)
>gi|1172527|sp|P45723|PLC_STAAU 1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC)
>gi|586104|sp|P37376|TNPF_STAAU TRANSPOSASE FOR TRANSPOSON TN554 HOMOLOG
>gi|586103|sp|P37375|TNPE_STAAU TRANSPOSASE B (TRANSPOSON TN554 HOMOLOG)
>gi|586027|sp|P38507|SPA2_STAAU IMMUNOGLOBULIN G BINDING PROTEIN A PRECURSOR (IGG BINDING PROTEIN A)
>gi|548620|sp|P17875|PTMA_STAAU PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL) (MANNITOL-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
>gi|548619|sp|PTMA_STAAU_2 [Segment 2 of 2] PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL) (MANNITOL-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
>gi|548618|sp|PTMA_STAAU_1 [Segment 1 of 2] PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL) (MANNITOL-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
>gi|400965|sp|P31337|RADC_STAAU DNA REPAIR PROTEIN RADC HOMOLOG (25 KD PROTEIN)
>gi|136146|sp|P06698|TRAC_STAAU TRANSPOSASE FOR TRANSPOSON TN554
>gi|136133|sp|P18416|TRA3_STAAU TRANSPOSASE FOR TRANSPOSON TN552 (ORF 480)
>gi|135956|sp|P06697|TNPB_STAAU TRANSPOSASE B (TRANSPOSON TN554)
>gi|135955|sp|P06696|TNPA_STAAU TRANSPOSASE A (TRANSPOSON TN554)
>gi|135949|sp|P19775|TRA6_STAAU TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS256 IN TRANSPOSON TN4001
>gi|135248|sp|P23736|T2S9_STAAU TYPE II RESTRICTION ENZYME SAU96I (ENDONUCLEASE SAU96I) (R.SAU96I)
>gi|135247|sp|P16667|T2S3_STAAU TYPE II RESTRICTION ENZYME SAU3AI (ENDONUCLEASE SAU3AI) (R.SAU3AI)
>gi|135003|sp|P04188|STSP_STAAU GLUTAMYL ENDOPEPTIDASE PRECURSOR (STAPHYLOCOCCAL SERINE PROTEINASE) (V8 PROTEINASE) (ENDOPROTEINASE GLU-C)
>gi|135002|sp|P12055|STR_STAAU STREPTOMYCIN RESISTANCE PROTEIN
>gi|134959|sp|P17855|STC2_STAAU STAPHYLOCOAGULASE PRECURSOR
>gi|134958|sp|P07767|STC1_STAAU STAPHYLOCOAGULASE PRECURSOR
>gi|134189|sp|P00802|SAK_STAAU STAPHYLOKINASE PRECURSOR (NEUTRAL PROTEINASE) (PROTEASE III)
>gi|134150|sp|P04827|S3AD_STAAU STREPTOMYCIN 3''-ADENYLYLTRANSFERASE (AAD(9))
>gi|133479|sp|P26766|RPSD_STAAU RNA POLYMERASE SIGMA FACTOR RPOD
>gi|133112|sp|P14491|RLX3_STAAU RLX PROTEIN
>gi|133111|sp|P03865|RLX2_STAAU RLX PROTEIN
>gi|133109|sp|P12054|RLX1_STAAU RLX PROTEIN
>gi|132380|sp|P08115|REP_STAAU REPLICATION INITIATION PROTEIN
>gi|132374|sp|P03858|REPY_STAAU REPLICATION PROTEIN
>gi|132372|sp|P03862|REPX_STAAU REP PROTEIN (REPLICATION PROTEIN) (READING FRAME A)
>gi|132369|sp|P19529|REPN_STAAU REPLICATION INITIATION PROTEIN
>gi|132368|sp|P14490|REPM_STAAU REPLICATION INITIATION PROTEIN
>gi|132364|sp|P12053|REPE_STAAU REPLICATION INITIATION PROTEIN
>gi|132362|sp|P03065|REPD_STAAU REPLICATION INITIATION PROTEIN
>gi|132361|sp|P03064|REPC_STAAU REPLICATION INITIATION PROTEIN (PROTEIN A)
>gi|132357|sp|P05061|REPB_STAAU REPLICATION PROTEIN
>gi|132322|sp|P13969|REMA_STAAU REPLICATION AND MAINTENANCE PROTEIN (PLASMID REPLICATION PROTEIN)
>gi|131518|sp|P02909|PTLA_STAAU PTS SYSTEM, LACTOSE-SPECIFIC IIA COMPONENT (EIIA-LAC) (LACTOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-LAC)
>gi|131497|sp|P11162|PTLB_STAAU PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT (EIIIB-LAC) (LACTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-LAC)
>gi|130085|sp|P09978|PHLC_STAAU PHOSPHOLIPASE C PRECURSOR (BETA-HEMOLYSIN) (BETA-TOXIN) (SPHINGOMYELINASE)
>gi|129676|sp|P07944|PBP_STAAU BETA-LACTAM-INDUCIBLE PENICILLIN-BINDING PROTEIN
>gi|129132|sp|P21223|OMP7_STAAU 70 KD OUTER MEMBRANE PROTEIN PRECURSOR
>gi|129123|sp|P21222|NP30_STAAU 30 KD NEUTRAL PHOSPHATASE (NPTASE)
>gi|128511|sp|P21191|NORA_STAAU QUINOLONE RESISTANCE NORA PROTEIN

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>gi|127486|sp|P23737|MTS9_STAAU MODIFICATION METHYLASE SAU96I (CYTOSINE-SPECIFIC METHYLTRANSFERASE SAU96I) (M.SAU96I)
>gi|127485|sp|P16668|MTS3_STAAU MODIFICATION METHYLASE SAU3AI (CYTOSINE-SPECIFIC METHYLTRANSFERASE SAU3AI) (M.SAU3AI)
>gi|6016606|sp|P068285|MSCL_STAAU LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL
>gi|6016162|sp|P034092|GSA_STAAU GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
>gi|4033454|sp|P72364|LEPH_STAAU INACTIVE SIGNAL PEPTIDASE IA
>gi|4033452|sp|P72365|LEP_STAAU SIGNAL PEPTIDASE IB (SPASE IB) (LEADER PEPTIDASE IB)
>gi|3122102|sp|P007325|FTSA_STAAU CELL DIVISION PROTEIN FTSA
>gi|1709003|sp|P50307|METK_STAAU S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
>gi|1708807|sp|P52282|LGT_STAAU PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE
>gi|1707902|sp|P31714|GHM2_STAAU GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
>gi|1707901|sp|GHM2_STAAU_2 [Segment 2 of 2] GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
>gi|1707900|sp|GHM2_STAAU_1 [Segment 1 of 2] GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
>gi|1346584|sp|P80544|MRSP_STAAU METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346583|sp|MRSP_STAAU_7 [Segment 7 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346582|sp|MRSP_STAAU_6 [Segment 6 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346581|sp|MRSP_STAAU_5 [Segment 5 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346580|sp|MRSP_STAAU_4 [Segment 4 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346579|sp|MRSP_STAAU_3 [Segment 3 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346578|sp|MRSP_STAAU_2 [Segment 2 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346577|sp|MRSP_STAAU_1 [Segment 1 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346244|sp|P20832|GYRB_STAAU DNA GYRASE SUBUNIT B
>gi|1346238|sp|P20831|GYRA_STAAU DNA GYRASE SUBUNIT A
>gi|1176137|sp|P45556|HRCA_STAAU HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
>gi|1169769|sp|P45498|FTSZ_STAAU CELL DIVISION PROTEIN FTSZ
>gi|547868|sp|P36884|LPCA_STAAU CHLORAMPHENICOL RESISTANCE LEADER PEPTIDE
>gi|400204|sp|P31716|LUKS_STAAU LEUKOCIDIN S SUBUNIT PRECURSOR
>gi|400203|sp|P31715|LUKF_STAAU LEUKOCIDIN F SUBUNIT PRECURSOR (GAMMA-HEMOLYSIN, H-GAMMA-I SUBUNIT)
>gi|127020|sp|P08656|MERT_STAAU MERCURY TRANSPORT PROTEIN (MERCURY ION TRANSPORT PROTEIN)
>gi|127015|sp|P22874|MERR_STAAU MERCURIC RESISTANCE OPERON REGULATORY PROTEIN
>gi|126999|sp|P08653|MERRB_STAAU ALKYL MERCURY LYASE (ORGANOMERCURIAL LYASE)
>gi|126995|sp|P08663|MERB_STAAU MERCURIC REDUCTASE (HG(II) REDUCTASE)
>gi|126940|sp|P26598|MCCI_STAAU METHICILLIN RESISTANCE REGULATORY PROTEIN MCCI
>gi|126446|sp|P03063|LPRM_STAAU 23S rRNA METHYLASE LEADER PEPTIDE (ERYTHROMYCIN RESISTANCE LEADER PEPTIDE)
>gi|126333|sp|P10335|LIP_STAAU LIPASE PRECURSOR (GLYCEROL ESTER HYDROLASE)
>gi|125937|sp|P16644|LACR_STAAU LACTOSE PHOSPHOTRANSFERASE SYSTEM REPRESSOR
>gi|125930|sp|P11175|LAGC_STAAU 6-PHOSPHO-BETA-GALACTOSIDASE (BETA-D-PHOSPHOGALACTOSIDE GALACTOHYDROLASE) (PGALASE) (P-BETA-GAL) (PBG)
>gi|125908|sp|P26594|LACA_STAAU GALACTOSE-6-PHOSPHATE ISOMERASE LACA SUBUNIT
>gi|125464|sp|P00554|KKA3_ENTFA AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (KANAMYCIN KINASE, TYPE III) (NEOMYCIN-KANAMYCIN PHOSPHOTRANSFERASE, TYPE III) (APH(3')III)
>gi|125191|sp|P05057|KANU_STAAU KANAMYCIN NUCLEOTIDYLTRANSFERASE (NEO(R))
>gi|123184|sp|P09616|HLA_STAAU ALPHA-HEMOLYSIN PRECURSOR (ALPHA-TOXIN) (ALPHA-HL)
>gi|6015099|sp|P069174|ENO_STAAU ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (LAMNIN BINDING PROTEIN)
>gi|6014977|sp|P059822|DLHD_STAAU DIHYDROLIPOAMIDE DEHYDROGENASE (E3 COMPONENT OF PYRUVATE COMPLEX) (MEMBRANE-BOUND RIBOSOME PROTEIN COMPLEX 50 KD SUBUNIT)
>gi|6014729|sp|P81684|CS40_STAAU 40 KD VITRONECTIN-BINDING CELL SURFACE PROTEIN
>gi|3023644|sp|P005701|DHPS_STAAU DIHYDROPTEROATE SYNTHASE (DIHYDROPTEROATE PYROPHOSPHORYLASE) (DHPS)
>gi|2829402|sp|P49994|DNAA_STAAU CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA
>gi|1706496|sp|P50029|DPB3_STAAU DNA POLYMERASE III, BETA CHAIN
>gi|1169381|sp|P45554|DNAK_STAAU DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70)
>gi|544199|sp|P10167|DYRB_STAAU DIHYDROFOLATE REDUCTASE TYPE I
>gi|462026|sp|P34071|ETC2_STAAU ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2)
>gi|127195|sp|P13978|ERM4_STAAU rRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
>gi|127194|sp|P13957|ERM3_STAAU rRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
>gi|127191|sp|P06699|ERM1_STAAU rRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
>gi|119903|sp|P14305|FEMB_STAAU POSSIBLE PROTEIN FEMB (ORF 419)
>gi|119902|sp|P14304|FEMA_STAAU FACTOR ESSENTIAL FOR EXPRESSION OF METHICILLIN RESISTANCE
>gi|119655|sp|P12993|ETXE_STAAU ENTEROTOXIN TYPE E PRECURSOR (SEE)
>gi|119654|sp|P20723|ETXD_STAAU ENTEROTOXIN TYPE D PRECURSOR (SED)
>gi|119653|sp|P01552|ETXB_STAAU ENTEROTOXIN TYPE B PRECURSOR (SEB)
>gi|119652|sp|P13163|ETXA_STAAU ENTEROTOXIN TYPE A PRECURSOR (SEA)
>gi|119626|sp|P23313|ETC3_STAAU ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3)
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>gi|119625|sp|P01553|ETC1_STAAU ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1)
>gi|119624|sp|P09332|ETB_STAAU EXFOLIATIVE TOXIN B PRECURSOR (EPIDERMOLYTIC TOXIN B)
>gi|119621|sp|P09331|ETA_STAAU EXFOLIATIVE TOXIN A PRECURSOR (EPIDERMOLYTIC TOXIN A)
>gi|119131|sp|P24121|EDIN_STAAU EPIDERMAL CELL DIFFERENTIATION INHIBITOR PRECURSOR (EDIN)
>gi|118976|sp|P13955|DYRA_STAAU DIHYDROFOLATE REDUCTASE TYPE I (TN4003)
>gi|5813905|gb|AAD52059.1|AF086783_7 glycerol esther hydrolase [Staphylococcus aureus]
>gi|5813904|gb|AAD52058.1|AF086783_6 IcaC [Staphylococcus aureus]
>gi|5813903|gb|AAD52057.1|AF086783_5 IcaB [Staphylococcus aureus]
>gi|5813902|gb|AAD52056.1|AF086783_4 IcaD [Staphylococcus aureus]
>gi|5813901|gb|AAD52055.1|AF086783_3 IcaA [Staphylococcus aureus]
>gi|5813900|gb|AAD52054.1|AF086783_2 IcaR [Staphylococcus aureus]
>gi|5813899|gb|AAD52053.1|AF086783_1 CapA [Staphylococcus aureus]
>gi|6002652|gb|AAF00080.1|AF095597_1 ferric uptake regulator homolog [Staphylococcus aureus]
>gi|6002650|gb|AAF00079.1|AF095596_1 ferric uptake regulator homolog [Staphylococcus aureus]
>gi|6002648|gb|AAF00078.1|AF095595_1 ferric uptake regulator homolog [Staphylococcus aureus]
>gi|3913259|sp|Q53654|CNA_STAAU COLLAGEN ADHESIN PRECURSOR
>gi|584919|sp|Q08841|CH10_STAAU 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 10)
>gi|116920|sp|P25921|COP6_STAAU COP-6 PROTEIN
>gi|1168660|sp|P20384|BIN3_STAAU POTENTIAL DNA-INVERTASE BIN3 (TRANSPOSON TN552)
>gi|729029|sp|P39861|CAPL_STAAU CAPL PROTEIN
>gi|729028|sp|P39860|CAPK_STAAU CAPK PROTEIN
>gi|729027|sp|P39859|CAPJ_STAAU CAPJ PROTEIN
>gi|729025|sp|P39857|CAPH_STAAU CAPH PROTEIN
>gi|729024|sp|P39856|CAPG_STAAU CAPG PROTEIN
>gi|729021|sp|P39855|CAPF_STAAU CAPF PROTEIN
>gi|729020|sp|P39854|CAPE_STAAU CAPE PROTEIN
>gi|729019|sp|P39853|CAPD_STAAU CAPD PROTEIN
>gi|729018|sp|P39852|CAPC_STAAU CAPC PROTEIN
>gi|729017|sp|P39851|CAPB_STAAU CAPB PROTEIN
>gi|729016|sp|P39850|CAPA_STAAU CAPA PROTEIN
>gi|584871|sp|P37374|CADF_STAAU CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG
>gi|584870|sp|P37386|CADD_STAAU PROBABLE CADMIUM-TRANSPORTING ATPASE (CADMIUM EFFLUX ATPASE)
>gi|543935|sp|P36883|CAT5_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
>gi|543934|sp|P36882|CAT4_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
>gi|231569|sp|P30338|ARSR_STAAU ARSENICAL RESISTANCE OPERON REPRESSOR
>gi|231567|sp|P30330|ARSC_STAAU ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER)
>gi|231565|sp|P30329|ARSB_STAAU ARSENICAL PUMP MEMBRANE PROTEIN
>gi|140340|sp|P20047|CADC_STAAU CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN
>gi|115688|sp|P06135|CAT3_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
>gi|115685|sp|P00486|CAT2_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
>gi|115680|sp|P00485|CAT1_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
>gi|115414|sp|P20021|CADA_STAAU PROBABLE CADMIUM-TRANSPORTING ATPASE (CADMIUM EFFLUX ATPASE)
>gi|115052|sp|P22491|BLE2_STAAU BLEOMYCIN RESISTANCE PROTEIN
>gi|115051|sp|P13014|BLE1_BACSP BLEOMYCIN RESISTANCE PROTEIN (BRP)
>gi|115049|sp|P18357|BLAR_STAAU REGULATORY PROTEIN BLAR1
>gi|115044|sp|P18415|BLAI_STAAU PENICILLINASE REPRESSOR (REGULATORY PROTEIN BLAI) (BETA-LACTAMASE REPRESSOR PROTEIN)
>gi|114996|sp|P19241|BINR_STAAU DNA-INVERTASE BINR (TRANSPOSON TN552)
>gi|114995|sp|P18358|BINL_STAAU TRANSPOSON TN552 RESOLVASE
>gi|114300|sp|P18179|ATBP_STAAU POTENTIAL ATP-BINDING PROTEIN (ORF 271)
>gi|3913011|sp|O05204|AHPF_STAAU ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F
>gi|113527|sp|P13131|AGRA_STAAU ACCESSORY GENE REGULATOR PROTEIN A
>gi|112954|sp|P14507|AACA_STAAU BIFUNCTIONAL AAC/APH [INCLUDES: 6'-AMINOGLYCOSIDE N-ACETYLTRANSFERASE (AAC(6'))]; 2''-AMINOGLYCOSIDE PHOSPHOTRANSFERASE (APH(2''))]
>gi|1729798|emb|CAA71069.1|CTORF239 [Staphylococcus aureus]
>gi|1729797|emb|CAA71068.1|sigma-B [Staphylococcus aureus]
>gi|1729796|emb|CAA71067.1|rsbW [Staphylococcus aureus]
>gi|1729795|emb|CAA71066.1|rsbV [Staphylococcus aureus]
>gi|1729794|emb|CAA71065.1|rsbU [Staphylococcus aureus]
>gi|1729793|emb|CAA71064.1|ORF136 [Staphylococcus aureus]
>gi|1729792|emb|CAA71063.1|ORF56 [Staphylococcus aureus]
>gi|5834651|emb|CAB55331.1|putative mannitol-specific IIA component [Staphylococcus aureus]
>gi|5834650|emb|CAB55330.1|putative mannitol-1-phosphate 5-dehydrogenase [Staphylococcus aureus]
>gi|5834649|emb|CAB55329.1|Mrp protein [Staphylococcus aureus]
>gi|5834648|emb|CAA71060.2|phosphoglucosamine mutase, GlmM [Staphylococcus aureus]
>gi|5834647|emb|CAB55328.1|hypothetical protein [Staphylococcus aureus]
>gi|5834646|emb|CAB55327.1|hypothetical protein [Staphylococcus aureus]
>gi|5834645|emb|CAB55326.1|arginase [Staphylococcus aureus]
>gi|4775551|emb|CAA71062.1|CTORF1365 [Staphylococcus aureus]
>gi|4775543|emb|CAA70781.1|arginase [Staphylococcus aureus]
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>gi|4775542|emb|CAA70780.1| ORF94 [Staphylococcus aureus]
>gi|46695|emb|CAA25094.1| protein A [Staphylococcus aureus]
>gi|5822514|pdb|3LKF|A Chain A, Leukocidin F (Hlgb) From Staphylococcus Aureus With Phosphocholine Bound
>gi|5822485|pdb|2LKF|A Chain A, Leukocidin F (Hlgb) From Staphylococcus Aureus
>gi|5822083|pdb|1LKF|A Chain A, Leukocidin F (Hlgb) From Staphylococcus Aureus
>gi|5822030|pdb|1CQV|A Chain A, Crystal Structure Of Staphylococcal Enterotoxin C2 At 100k
>gi|5739084|gb|AAD50329.1|AF077865_1 beta-lactamase [Staphylococcus aureus]
>gi|5726436|gb|AAD48437.1|AF162687_1 sortase [Staphylococcus aureus]
>gi|5726302|gb|AAD48404.1|AF129010_3 CsbB homolog [Staphylococcus aureus]
>gi|5726301|gb|AAD48403.1|AF129010_2 histidine protein kinase SaeS [Staphylococcus aureus]
>gi|5726300|gb|AAD48402.1|AF129010_1 response regulator SaeR [Staphylococcus aureus]
>gi|5690277|gb|AAD47014.1|AF147744_4 transporter [Staphylococcus aureus]
>gi|5690276|gb|AAD47013.1|AF147744_3 lantibiotic modifying enzyme [Staphylococcus aureus]
>gi|5690275|gb|AAD47012.1|AF147744_2 lantibiotic structural protein beta [Staphylococcus aureus]
>gi|5690274|gb|AAD47011.1|AF147744_1 lantibiotic structural protein alpha [Staphylococcus aureus]
>gi|5672689|dbj|BAA13059.2| D-alanine-D-alanyl carrier protein ligase [Staphylococcus aureus]
>gi|1405338|dbj|BAA13062.1| extramembranal protein [Staphylococcus aureus]
>gi|1405337|dbj|BAA13061.1| D-alanyl carrier protein [Staphylococcus aureus]
>gi|1405336|dbj|BAA13060.1| hypothethcal membrane transporter [Staphylococcus aureus]
>gi|1405334|dbj|BAA13058.1| unknown [Staphylococcus aureus]
>gi|5679714|emb|CAB51807.1| cell surface protein map-w [Staphylococcus aureus]
>gi|5531420|emb|CAB50920.1| map-7 protein [Staphylococcus aureus]
>gi|4558750|gb|AAD22731.1| heat shock protein 60 kDa [Staphylococcus aureus]
>gi|4558748|gb|AAD22730.1| heat shock protein 60 kDa [Staphylococcus aureus]
>gi|4558746|gb|AAD22729.1| heat shock protein 60 kDa [Staphylococcus aureus]
>gi|4558744|gb|AAD22728.1| heat shock protein 60 kDa [Staphylococcus aureus]
>gi|4558742|gb|AAD22727.1| heat shock protein 60 kDa [Staphylococcus aureus]
>gi|4558740|gb|AAD22726.1| heat shock protein 60 kDa [Staphylococcus aureus]
>gi|4558738|gb|AAD22725.1| heat shock protein 60 kDa [Staphylococcus aureus]
>gi|4558736|gb|AAD22724.1| heat shock protein 60 kDa [Staphylococcus aureus]
>gi|4558706|gb|AAD22709.1| heat shock protein 60 [Staphylococcus aureus subsp. aureus]
>gi|4558704|gb|AAD22708.1| heat shock protein 60 [Staphylococcus aureus subsp. anaerobius]
>gi|4205743|gb|AAD11256.1| heat shock protein 60 [Staphylococcus aureus]
>gi|5542332|pdb|1PVL| Structure Of The Pantone-Valentine Leucocidin F Component From Staphylococcus Aureus
>gi|2642659|gb|AAB87090.1| UDP-N-acetylmuramoyl-L-alanine synthetase [Staphylococcus aureus]
>gi|1916729|gb|AAB51227.1| CadD [Staphylococcus aureus]
>gi|5441303|gb|AAD43176.1|AF098801_1 penicillin-binding protein Pbp2b [Staphylococcus aureus]
>gi|581566|emb|CAA45142.1| mecR1 [Staphylococcus aureus]
>gi|46615|emb|CAA45143.1| mecI [Staphylococcus aureus]
>gi|46613|emb|CAA45141.1| mecA [Staphylococcus aureus]
>gi|5391440|dbj|BAA82253.1| orf2 [Staphylococcus aureus]
>gi|5391439|dbj|BAA82252.1| orfX [Staphylococcus aureus]
>gi|5391438|dbj|BAA82251.1| orf3 [Staphylococcus aureus]
>gi|5391437|dbj|BAA82250.1| orf1 [Staphylococcus aureus]
>gi|5327232|emb|CAB46341.1| adenine methylase [Staphylococcus aureus]
>gi|5327231|emb|CAB46340.1| adenine methaylase [Staphylococcus aureus]
>gi|5327230|emb|CAB46339.1| hypothetical protein [Staphylococcus aureus]
>gi|5114231|gb|AAD40238.1|AF136709_2 histidine kinase YycG [Staphylococcus aureus]
>gi|5114230|gb|AAD40237.1|AF136709_1 response regulator YycF [Staphylococcus aureus]
>gi|3767595|dbj|BAA33858.1| ORF4 [Staphylococcus aureus]
>gi|3767594|dbj|BAA33857.1| Eprh [Staphylococcus aureus]
>gi|3767593|dbj|BAA33856.1| LytN [Staphylococcus aureus]
>gi|3767592|dbj|BAA33855.1| ORF1 [Staphylococcus aureus]
>gi|2605638|gb|AAB84174.1| staphylokinase [Staphylococcus aureus]
>gi|5031413|gb|AAD38159.1|AF151117_1 replication protein [Staphylococcus aureus]
>gi|4930180|pdb|2DHN| Complex Of 7,8-Dihydroneopterin Aldolase From Staphylococcus Aureus With 6-Hydroxymethyl-7,8-Dihydropterin At 2.2 A Resolution
>gi|4930033|pdb|1DHN| 1.65 Angstrom Resolution Structure Of 7,8-Dihydroneopterin Aldolase From Staphylococcus Aureus
>gi|4929299|gb|AAD33940.1|AF144661_1 factor essential for methicillin resistance [Staphylococcus aureus subsp. anaerobius]
>gi|3892895|emb|CAA75651.1| phosphoglucosamine-mutase [Staphylococcus aureus]
>gi|3892894|emb|CAA75650.1| hypothetical protein [Staphylococcus aureus]
>gi|3892893|emb|CAA75649.1| hypothetical protein [Staphylococcus aureus]
>gi|3892892|emb|CAA75648.1| arginase [Staphylococcus aureus]
>gi|4115707|dbj|BAA36484.1| NorA [Staphylococcus aureus]
>gi|4582216|emb|CAB40191.1| elongation factor G (EF-G) [Staphylococcus aureus]
>gi|4574238|gb|AAD23963.1|AF106851_2 FmhC [Staphylococcus aureus]
>gi|4574237|gb|AAD23962.1|AF106851_1 LytN [Staphylococcus aureus]

>gi|4574235|gb|AAD23961.1|AF106850_1 FmhB [Staphylococcus aureus]
>gi|4574233|gb|AAD23960.1|AF106849_1 FmhA [Staphylococcus aureus]
>gi|4572581|gb|AAD15142.2| Unknown [Staphylococcus aureus]
>gi|3891901|pdb|1CV8| Staphopain, Cysteine Proteinase From Staphylococcus Aureus V8
>gi|2981905|pdb|3NUC| Staphylococcal Nuclease, 1-N-Propane Thiol Disulfide To V23c Variant
>gi|2981899|pdb|2NUC| Staphylococcal Nuclease, Ethane Thiol Disulfide To V23c Variant
>gi|1942332|pdb|1SNQ| Protein Stability In Staphylococcal Nuclease
>gi|1942331|pdb|1SNP| Protein Stability In Staphylococcal Nuclease
>gi|1942330|pdb|1SNO| Protein Stability In Staphylococcal Nuclease
>gi|4139848|pdb|1SSN| Staphylokinase, Sakstar Variant, Nmr, 20 Structures
>gi|4139648|pdb|1TS5|B Chain B, I140t Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139647|pdb|1TS5|A Chain A, I140t Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139646|pdb|1TS4|B Chain B, Q139k Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139645|pdb|1TS4|A Chain A, Q139k Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139644|pdb|1TS3|C Chain C, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139643|pdb|1TS3|B Chain B, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139642|pdb|1TS3|A Chain A, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139641|pdb|1TS2|C Chain C, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139640|pdb|1TS2|B Chain B, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139639|pdb|1TS2|A Chain A, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|3891592|pdb|1AW7|D Chain D, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|3891591|pdb|1AW7|C Chain C, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|3891590|pdb|1AW7|B Chain B, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|3891589|pdb|1AW7|A Chain A, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4454324|emb|CAA10802.1| MapN protein [Staphylococcus aureus]
>gi|3970797|emb|CAA74099.1| polynucleotide phosphorylase [Staphylococcus aureus]
>gi|4530244|gb|AAD21960.1| putative exoprotein DltD [Staphylococcus aureus]
>gi|4530243|gb|AAD21959.1| D-alanine carrier protein DltC [Staphylococcus aureus]
>gi|4530242|gb|AAD21958.1| putative membrane protein DltB [Staphylococcus aureus]
>gi|4530241|gb|AAD21957.1| D-alanine-D-alanyl carrier protein ligase DltA [Staphylococcus aureus]
>gi|4530240|gb|AAD21956.1| unknown [Staphylococcus aureus]
>gi|4490615|emb|CAB38647.1| triosephosphate isomerase [Staphylococcus aureus]
>gi|4490614|emb|CAB38646.1| phosphoglycerate kinase [Staphylococcus aureus]
>gi|4490613|emb|CAB38645.1| glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus]
>gi|4490612|emb|CAB38644.1| gap regulator [Staphylococcus aureus]
>gi|4490610|emb|CAB38643.1| ribonucleotide reductase minor subunit [Staphylococcus aureus]
>gi|4490609|emb|CAB38642.1| ribonucleotide reductase major subunit [Staphylococcus aureus]
>gi|4490608|emb|CAB38641.1| NRD1 [Staphylococcus aureus]
>gi|4454322|emb|CAA10788.1| hypothetical protein [Staphylococcus aureus]
>gi|4454321|emb|CAA10787.1| hypothetical protein [Staphylococcus aureus]
>gi|4126675|dbj|BAA36689.1| Hypothetical protein [Staphylococcus aureus]
>gi|4126674|dbj|BAA36688.1| Hypothetical protein [Staphylococcus aureus]
>gi|4126673|dbj|BAA36687.1| CzcA [Staphylococcus aureus]
>gi|4126672|dbj|BAA36686.1| czcD [Staphylococcus aureus]
>gi|4126671|dbj|BAA36685.1| Hypothetical protein [Staphylococcus aureus]
>gi|4001731|dbj|BAA35101.1| MnhG [Staphylococcus aureus]
>gi|4001730|dbj|BAA35100.1| MnhF [Staphylococcus aureus]
>gi|4001729|dbj|BAA35099.1| MnhE [Staphylococcus aureus]
>gi|4001728|dbj|BAA35098.1| MnhD [Staphylococcus aureus]
>gi|4001727|dbj|BAA35097.1| MnhC [Staphylococcus aureus]
>gi|4001726|dbj|BAA35096.1| MnhB [Staphylococcus aureus]
>gi|4001725|dbj|BAA35095.1| MnhA [Staphylococcus aureus]
>gi|4001724|dbj|BAA35094.1| OrfA [Staphylococcus aureus]
>gi|3694944|gb|AAC62498.1| SirC [Staphylococcus aureus]
>gi|3694943|gb|AAC62497.1| SirB [Staphylococcus aureus]
>gi|3694942|gb|AAC62496.1| lipoprotein SirA [Staphylococcus aureus]
>gi|4138456|emb|CAA11555.1| Map protein [Staphylococcus aureus]
>gi|4138445|emb|CAA77018.1| adenine methylase [Staphylococcus aureus]
>gi|3955031|emb|CAA76853.1| PBP2 [Staphylococcus aureus]
>gi|3955030|emb|CAA76852.1| unknown [Staphylococcus aureus]
>gi|3550596|emb|CAA06652.1| sdr E [Staphylococcus aureus]
>gi|3550594|emb|CAA06651.1| sdrD [Staphylococcus aureus]
>gi|3550592|emb|CAA06650.1| sdrC [Staphylococcus aureus]
>gi|809080|emb|CAA24595.1| reading frame [Staphylococcus aureus]
>gi|3320606|gb|AAD09875.1| putative heme A synthase [Staphylococcus aureus]
>gi|4104230|gb|AAD01977.1| phospho-N-acetylmuramoyl-pentapeptide translocase [Staphylococcus aureus]
>gi|4103900|gb|AAD01884.1| 60 kDa heat shock protein [Staphylococcus aureus]
>gi|4097757|gb|AAD00167.1| lytic regulatory protein [Staphylococcus aureus]
>gi|4090655|gb|AAC98834.1| ORF64 [Staphylococcus aureus]
>gi|4090654|gb|AAC98833.1| replication protein [Staphylococcus aureus]
>gi|4090652|gb|AAC98832.1| ORF64 [Staphylococcus aureus]

>gi|4090651|gb|AAC98831.1| replication protein [Staphylococcus aureus]
>gi|2811118|gb|AAC95492.1| unknown [Staphylococcus aureus]
>gi|2811115|gb|AAC95491.1| unknown [Staphylococcus aureus]
>gi|4009497|gb|AAC95464.1| cell division protein DivIVA [Staphylococcus aureus]
>gi|4009496|gb|AAC95463.1| YlmH [Staphylococcus aureus]
>gi|4009495|gb|AAC95462.1| YlmG [Staphylococcus aureus]
>gi|4009494|gb|AAC95461.1| YlmF [Staphylococcus aureus]
>gi|4009493|gb|AAC95460.1| YlmE [Staphylococcus aureus]
>gi|4009492|gb|AAC95459.1| YlmD [Staphylococcus aureus]
>gi|4009491|gb|AAC95458.1| cell division protein FtsZ [Staphylococcus aureus]
>gi|1402771|gb|AAC80254.1| major cold-shock protein [Staphylococcus aureus]
>gi|3372542|gb|AAC78590.1| enterotoxin J [Staphylococcus aureus]
>gi|3372541|gb|AAC78589.1| enterotoxin D [Staphylococcus aureus]
>gi|3892644|dbj|BAA34540.1| MphBM [Staphylococcus aureus]
>gi|3892643|dbj|BAA34539.1| MsrSA [Staphylococcus aureus]
>gi|3892642|dbj|BAA34538.1| leader peptide [Staphylococcus aureus]
>gi|3850852|emb|CAA76222.1| hypothetical protein [Staphylococcus aureus]
>gi|3850851|emb|CAA76221.1| alr protein [Staphylococcus aureus]
>gi|3850850|emb|CAA76220.1| dpj protein [Staphylococcus aureus]
>gi|3850849|emb|CAA76219.1| hypothetical protein [Staphylococcus aureus]
>gi|3850848|emb|CAA76218.1| hypothetical protein [Staphylococcus aureus]
>gi|3850847|emb|CAA76217.1| hypothetical protein [Staphylococcus aureus]
>gi|3850846|emb|CAA76216.1| kpdC protein [Staphylococcus aureus]
>gi|3800828|gb|AAC69846.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
>gi|3800827|gb|AAC69845.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
>gi|3800826|gb|AAC69844.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
>gi|3800825|gb|AAC69843.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
>gi|3800823|gb|AAC69842.1| unknown [Staphylococcus aureus]
>gi|3800822|gb|AAC69841.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
>gi|3800821|gb|AAC69840.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
>gi|3800820|gb|AAC69839.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
>gi|3800819|gb|AAC69838.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
>gi|3800818|gb|AAC69837.1| oligopeptide transporter putative substrate binding domain [Staphylococcus aureus]
>gi|2765304|emb|CAA73668.1| leukotoxin, LukD [Staphylococcus aureus]
>gi|2765303|emb|CAA73667.1| leukotoxin LukE [Staphylococcus aureus]
>gi|3212829|pdb|5NUC| Staphylococcal Nuclease, 1-N-Pentane Thiol Disulfide To V23c Variant
>gi|3212819|pdb|3SEB| Staphylococcal Enterotoxin B
>gi|2982145|pdb|2SAK| Staphylokinase (Sakstar Variant)
>gi|2914575|pdb|7AHL|G Chain G, Alpha-Hemolysin From Staphylococcus Aureus
>gi|2914574|pdb|7AHL|F Chain F, Alpha-Hemolysin From Staphylococcus Aureus
>gi|2914573|pdb|7AHL|E Chain E, Alpha-Hemolysin From Staphylococcus Aureus
>gi|2914572|pdb|7AHL|D Chain D, Alpha-Hemolysin From Staphylococcus Aureus
>gi|2914571|pdb|7AHL|C Chain C, Alpha-Hemolysin From Staphylococcus Aureus
>gi|2914570|pdb|7AHL|B Chain B, Alpha-Hemolysin From Staphylococcus Aureus
>gi|2914569|pdb|7AHL|A Chain A, Alpha-Hemolysin From Staphylococcus Aureus
>gi|2914205|pdb|2SEB|D Chain D, X-Ray Crystal Structure Of Hla-Dr4 Complexed With A Peptide From Human Collagen Ii
>gi|2780937|pdb|5TSS|B Chain B, Toxic Shock Syndrome Toxin-1: Orthorhombic P222(1) Crystal Form
>gi|2780936|pdb|5TSS|A Chain A, Toxic Shock Syndrome Toxin-1: Orthorhombic P222(1) Crystal Form
>gi|2780930|pdb|4TSS| Toxic Shock Syndrome Toxin-1: Tetragonal P4(1)2(1)2 Crystal Form
>gi|2780925|pdb|3TSS| Toxic Shock Syndrome Toxin-1 Tetramutant, P2(1) Crystal Form
>gi|2780919|pdb|2TSS|C Chain C, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
>gi|2780918|pdb|2TSS|B Chain B, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
>gi|2780917|pdb|2TSS|A Chain A, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
>gi|2392714|pdb|2QIL|C Chain C, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
>gi|2392713|pdb|2QIL|B Chain B, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
>gi|2392712|pdb|2QIL|A Chain A, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
>gi|1310952|pdb|2SOB| Sn-Ob, Ob-Fold Sub-Domain Of Staphylococcal Nuclease, Nmr, 10 Structures
>gi|2781288|pdb|1SXT|B Chain B, Staphylococcal Enterotoxin Type A (Sea) Co-Crystallised With Zinc
>gi|2781287|pdb|1SXT|A Chain A, Staphylococcal Enterotoxin Type A (Sea) Co-Crystallised With Zinc
>gi|2624726|pdb|1SE4| Staphylococcal Enterotoxin B Complexed With Lactose
>gi|2392546|pdb|1SE3| Staphylococcal Enterotoxin B Complexed With Gm3 Trisaccharide

>gi|2098291|pdb|1SNS|Chain B, Staphylococcal Nuclease Dimer Containing A Deletion Of Residues 114-119 Complexed With Calcium Chloride And The Competitive Inhibitor Deoxythymidine-3',5'-Diphosphate
>gi|2098290|pdb|1SND|A Chain A, Staphylococcal Nuclease Dimer Containing A Deletion Of Residues 114-119 Complexed With Calcium Chloride And The Competitive Inhibitor Deoxythymidine-3',5'-Diphosphate
>gi|1942753|pdb|1STB| Staphylococcal Enterotoxin C2 From Staphylococcus Aureus
>gi|1633348|pdb|1SEB|H Chain H, Complex Of The Human Mhc Class Ii Glycoprotein Hla-Dr1 And The Bacterial Superantigen Seb
>gi|1633344|pdb|1SEB|D Chain D, Complex Of The Human Mhc Class Ii Glycoprotein Hla-Dr1 And The Bacterial Superantigen Seb
>gi|1431724|pdb|1SE2| Staphylococcal Enterotoxin C2, Monoclinic Form
>gi|3212584|pdb|1OME|B Chain B, Crystal Structure Of The Omega Loop Deletion Mutant (Residues 163 - 178 Deleted) Of Beta-Lactamase From Staphylococcus Aureus Pcl
>gi|3212583|pdb|1OME|A Chain A, Crystal Structure Of The Omega Loop Deletion Mutant (Residues 163 - 178 Deleted) Of Beta-Lactamase From Staphylococcus Aureus Pcl
>gi|2392515|pdb|1QIL|C Chain C, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
>gi|2392514|pdb|1QIL|B Chain B, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
>gi|2392513|pdb|1QIL|A Chain A, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
>gi|2392479|pdb|1NUC| Staphylococcal Nuclease, V23c Variant
>gi|2624537|pdb|1JCK|D Chain D, T-Cell Receptor Beta Chain Complexed With Sec3 Superantigen
>gi|2624535|pdb|1JCK|B Chain B, T-Cell Receptor Beta Chain Complexed With Sec3 Superantigen
>gi|2098496|pdb|1KGE| Structure Of Beta-Lactamase Asn 170 Met Mutant
>gi|1942204|pdb|1KGF| Structure Of Beta-Lactamase Asn 170 Gln Mutant
>gi|1827772|pdb|1KNY|B Chain B, Kanamycin Nucleotidyltransferase
>gi|1827771|pdb|1KNY|A Chain A, Kanamycin Nucleotidyltransferase
>gi|2982092|pdb|1EXF|A Chain A, Exfoliative Toxin A
>gi|2098519|pdb|1EDL| Staphylococcal Protein A E-Domain (-60), Nmr, 22 Structures
>gi|2098517|pdb|1EDI| Staphylococcal Protein A E-Domain (180), Nmr, Minimized Average Structure
>gi|2098516|pdb|1EDJ| Staphylococcal Protein A E-Domain (180), Nmr, 20 Structures
>gi|2098515|pdb|1EDK| Staphylococcal Protein A E-Domain (-60), Nmr, Minimized Average Structure
>gi|1942144|pdb|1DJC| Structure Of Beta-Lactamase Precursor, S70a Mutant, At 120k
>gi|1942143|pdb|1DJB| Structure Of Beta-Lactamase Precursor, S70a Mutant, At 298k
>gi|1942142|pdb|1DJA| Structure Of Beta-Lactamase Precursor, K73h Mutant, At 298k
>gi|1633233|pdb|1ESF|B Chain B, Staphylococcal Enterotoxin A
>gi|1633232|pdb|1ESF|A Chain A, Staphylococcal Enterotoxin A
>gi|1942696|pdb|1BDD| Staphylococcus Aureus Protein A, Immunoglobulin-Binding B Domain, Nmr, Minimized Average Structure
>gi|1942695|pdb|1BDC| Staphylococcus Aureus Protein A, Immunoglobulin-Binding B Domain, Nmr, 10 Structures
>gi|3318765|pdb|1AMX| Collagen-Binding Domain From A Staphylococcus Aureus Adhesin
>gi|3212427|pdb|1AD4|B Chain B, Dihydropteroate Synthetase Complexed With Oh-Ch2-Pterin-Pyrophosphate From Staphylococcus Aureus
>gi|3212426|pdb|1AD4|A Chain A, Dihydropteroate Synthetase Complexed With Oh-Ch2-Pterin-Pyrophosphate From Staphylococcus Aureus
>gi|3212425|pdb|1AD1|B Chain B, Dihydropteroate Synthetase (Apo Form) From Staphylococcus Aureus
>gi|3212424|pdb|1AD1|A Chain A, Dihydropteroate Synthetase (Apo Form) From Staphylococcus Aureus
>gi|2554719|pdb|1AGJ|B Chain B, Epidermolytic Toxin A From Staphylococcus Aureus
>gi|2554718|pdb|1AGJ|A Chain A, Epidermolytic Toxin A From Staphylococcus Aureus
>gi|2554635|pdb|1ALQ| Circularly Permuted Beta-Lactamase From Staphylococcus Aureus Pcl
>gi|2392077|pdb|1AEX| Staphylococcal Nuclease, Methane Thiol Disulfide To V23c Variant
>gi|3212327|pdb|1A3V| Staphylococcal Nuclease, Cyclopentane Thiol Disulfide To V23c Variant
>gi|3212326|pdb|1A3U| Staphylococcal Nuclease, Cyclohexane Thiol Disulfide To V23c Variant
>gi|3212325|pdb|1A3T| Staphylococcal Nuclease, V23c Variant, Complex With 2-Fluoroethane Thiol And 3',5'-Thymidine Diphosphate
>gi|3212274|pdb|1A2U| Staphylococcal Nuclease, V23c Variant, Complex With 1-N-Butane Thiol And 3',5'-Thymidine Diphosphate
>gi|3212273|pdb|1A2T| Staphylococcal Nuclease, B-Mercaptoethanol Disulfide To V23c Variant
>gi|3776113|emb|CAA11406.1| succinate dehydrogenase complex, cytochrome b558 subunit [Staphylococcus aureus]
>gi|3776112|emb|CAA11405.1| excinuclease ABC, subunit C [Staphylococcus aureus]
>gi|3776111|emb|CAA11404.1| thioredoxin [Staphylococcus aureus]
>gi|3776110|emb|CAA11403.1| Muts-like protein [Staphylococcus aureus]
>gi|3747042|gb|AAC64162.1| tyrosine recombinase XerD [Staphylococcus aureus]
>gi|3676411|gb|AAC63227.1| putative transposase TnpE [Staphylococcus aureus]
>gi|3676410|gb|AAC63226.1| thymidylate synthetase ThyE [Staphylococcus aureus]
>gi|3676409|gb|AAC63225.1| trimethoprim resistance protein DfrA [Staphylococcus aureus]
>gi|3676408|gb|AAC63224.1| unknown [Staphylococcus aureus]
>gi|3676407|gb|AAC63223.1| putative transposase TnpD [Staphylococcus aureus]
>gi|3676406|gb|AAC63222.1| replication protein Rep [Staphylococcus aureus]
>gi|3676405|gb|AAC63221.1| putative transposase TnpC [Staphylococcus aureus]
>gi|3676456|gb|AAC61974.1| putative transposase TnpG [Staphylococcus aureus]
>gi|3676455|gb|AAC61973.1| putative transposase TnpF [Staphylococcus aureus]

>gi|3676454|gb|AAC61972.1| bifunctional aminoglycoside modifying enzyme AacA-AphD [Staphylococcus aureus]
>gi|3676453|gb|AAC61971.1| unknown [Staphylococcus aureus]
>gi|3676452|gb|AAC61970.1| putative transposase TnpE [Staphylococcus aureus]
>gi|3676451|gb|AAC61969.1| multidrug resistance efflux protein Smr [Staphylococcus aureus]
>gi|3676450|gb|AAC61968.1| putative replication initiation protein Rep(RC) [Staphylococcus aureus]
>gi|3676449|gb|AAC61967.1| putative transposase TnpD [Staphylococcus aureus]
>gi|3676448|gb|AAC61966.1| unknown [Staphylococcus aureus]
>gi|3676447|gb|AAC61965.1| putative single-stranded DNA binding protein TraM [Staphylococcus aureus]
>gi|3676446|gb|AAC61964.1| putative membrane protein TraL [Staphylococcus aureus]
>gi|3676445|gb|AAC61963.1| putative membrane protein TraK [Staphylococcus aureus]
>gi|3676444|gb|AAC61962.1| putative membrane protein TraJ [Staphylococcus aureus]
>gi|3676443|gb|AAC61961.1| putative topoisomerase TraI [Staphylococcus aureus]
>gi|3676442|gb|AAC61960.1| lipoprotein TraH [Staphylococcus aureus]
>gi|3676441|gb|AAC61959.1| putative membrane protein TraG [Staphylococcus aureus]
>gi|3676440|gb|AAC61958.1| putative membrane protein TraF [Staphylococcus aureus]
>gi|3676439|gb|AAC61957.1| putative ATPase TraE [Staphylococcus aureus]
>gi|3676438|gb|AAC61956.1| TraD [Staphylococcus aureus]
>gi|3676437|gb|AAC61955.1| putative membrane protein TraC [Staphylococcus aureus]
>gi|3676436|gb|AAC61954.1| putative membrane protein TraB [Staphylococcus aureus]
>gi|3676435|gb|AAC61953.1| TraA [Staphylococcus aureus]
>gi|3676434|gb|AAC61952.1| putative regulator of transfer genes ArtA [Staphylococcus aureus]
>gi|3676433|gb|AAC61951.1| putative transposase TnpC [Staphylococcus aureus]
>gi|3676432|gb|AAC61950.1| aminoglycoside adenyltransferase AadD [Staphylococcus aureus]
>gi|3676431|gb|AAC61949.1| bleomycin resistance protein Ble [Staphylococcus aureus]
>gi|3676430|gb|AAC61948.1| Pre [Staphylococcus aureus]
>gi|3676429|gb|AAC61947.1| putative transposase TnpB [Staphylococcus aureus]
>gi|3676428|gb|AAC61946.1| membrane protein [Staphylococcus aureus]
>gi|3676427|gb|AAC61945.1| putative transposase TnpA [Staphylococcus aureus]
>gi|3676426|gb|AAC61944.1| putative replication initiation protein Rep [Staphylococcus aureus]
>gi|3676425|gb|AAC61943.1| unknown [Staphylococcus aureus]
>gi|3676424|gb|AAC61942.1| unknown [Staphylococcus aureus]
>gi|3676423|gb|AAC61941.1| unknown [Staphylococcus aureus]
>gi|3676422|gb|AAC61940.1| putative membrane protein [Staphylococcus aureus]
>gi|3676421|gb|AAC61939.1| unknown [Staphylococcus aureus]
>gi|3676420|gb|AAC61938.1| oriT nickase Nes [Staphylococcus aureus]
>gi|3676419|gb|AAC61937.1| LtrC-like protein [Staphylococcus aureus]
>gi|3676418|gb|AAC61936.1| unknown [Staphylococcus aureus]
>gi|3676417|gb|AAC61935.1| unknown [Staphylococcus aureus]
>gi|3676416|gb|AAC61934.1| putative resolvase Res [Staphylococcus aureus]
>gi|3676415|gb|AAC61933.1| unknown [Staphylococcus aureus]
>gi|3676414|gb|AAC61932.1| unknown [Staphylococcus aureus]
>gi|3676413|gb|AAC61931.1| unknown [Staphylococcus aureus]
>gi|410007|gb|AAC60446.1| leukocidin F component [Staphylococcus aureus, MRSA No. 4, Peptide, 323 aa]
>gi|410006|gb|AAC60445.1| leukocidin S component [Staphylococcus aureus, MRSA No. 4, Peptide, 315 aa]
>gi|410005|gb|AAC60444.1| gamma-hemolysin II, H gamma II [Staphylococcus aureus, MRSA No. 4, Peptide, 309 aa]
>gi|2271510|gb|AAC46291.1| UDP-N-acetylmuramoyl-L-alanine : D-glutamate ligase; MurD [Staphylococcus aureus]
>gi|1773355|gb|AAC46099.1| Cap5P [Staphylococcus aureus]
>gi|1773354|gb|AAC46098.1| Cap5O [Staphylococcus aureus]
>gi|1773353|gb|AAC46097.1| Cap5N [Staphylococcus aureus]
>gi|1773352|gb|AAC46096.1| Cap5M [Staphylococcus aureus]
>gi|1773351|gb|AAC46095.1| Cap5L [Staphylococcus aureus]
>gi|1773350|gb|AAC46094.1| Cap5K [Staphylococcus aureus]
>gi|1773349|gb|AAC46093.1| Cap5J [Staphylococcus aureus]
>gi|1773348|gb|AAC46092.1| Cap5I [Staphylococcus aureus]
>gi|1773347|gb|AAC46091.1| Cap5H [Staphylococcus aureus]
>gi|1773346|gb|AAC46090.1| Cap5G [Staphylococcus aureus]
>gi|1773345|gb|AAC46089.1| Cap5F [Staphylococcus aureus]
>gi|1773344|gb|AAC46088.1| Cap5E [Staphylococcus aureus]
>gi|1773343|gb|AAC46087.1| Cap5D [Staphylococcus aureus]
>gi|1773342|gb|AAC46086.1| Cap5C [Staphylococcus aureus]
>gi|1773341|gb|AAC46085.1| Cap5B [Staphylococcus aureus]
>gi|1773340|gb|AAC46084.1| Cap5A [Staphylococcus aureus]
>gi|1673629|gb|AAC46100.1| O-acetyl transferase [Staphylococcus aureus]
>gi|706922|gb|AAC46354.1| ribosomal protein S7 [Staphylococcus aureus]
>gi|706921|gb|AAC46353.1| ribosomal protein S12 [Staphylococcus aureus]
>gi|706920|gb|AAC46352.1| unknown [Staphylococcus aureus]

>gi|2589184|gb|AAC45836.1| GSA-1-aminotransferase [Staphylococcus aureus]
>gi|2589183|gb|AAC45835.1| d-aminolevulinic acid dehydratase [Staphylococcus aureus]
>gi|2589182|gb|AAC45834.1| uroporphyrinogen III synthase [Staphylococcus aureus]
>gi|2589181|gb|AAC45833.1| porphobilinogen deaminase [Staphylococcus aureus]
>gi|2149898|gb|AAC45629.1| cell division protein [Staphylococcus aureus]
>gi|2149897|gb|AAC45628.1| cell division protein [Staphylococcus aureus]
>gi|2149896|gb|AAC45627.1| cell division protein [Staphylococcus aureus]
>gi|2149895|gb|AAC45626.1| D-glutamic acid adding enzyme [Staphylococcus aureus]
>gi|2149894|gb|AAC45625.1| phospho-N-muramic acid-pentapeptide translocase [Staphylococcus aureus]
>gi|2149893|gb|AAC45624.1| penicillin-binding protein 1 [Staphylococcus aureus]
>gi|2149892|gb|AAC45623.1| cell division protein [Staphylococcus aureus]
>gi|2149891|gb|AAC45622.1| unknown [Staphylococcus aureus]
>gi|2149890|gb|AAC45621.1| unknown [Staphylococcus aureus]
>gi|1314302|gb|AAC45357.1| isoleucyl-tRNA synthetase [Staphylococcus aureus]
>gi|1314301|gb|AAC45356.1| unknown [Staphylococcus aureus]
>gi|1575026|gb|AAC44840.1| LrgB
>gi|1575025|gb|AAC44839.1| holin-like protein LrgA
>gi|710422|gb|AAC44803.1| cmp-binding-factor 1
>gi|710421|gb|AAC44802.1| unknown
>gi|1595810|gb|AAC44435.1| type-I signal peptidase SpsB [Staphylococcus aureus]
>gi|1595809|gb|AAC44434.1| type-I signal peptidase SpsA [Staphylococcus aureus]
>gi|1397239|gb|AAC44135.1| elastin binding protein
>gi|1001961|gb|AAC43470.1| MHC class II analog
>gi|3327949|gb|AAC38785.1| putative recombinase Sin [Staphylococcus aureus]
>gi|3327948|gb|AAC38784.1| multidrug efflux protein QacB [Staphylococcus aureus]
>gi|3327947|gb|AAC38783.1| transcriptional regulator QacR [Staphylococcus aureus]
>gi|3327945|gb|AAC38782.1| putative transposase TnpA [Staphylococcus aureus]
>gi|3327944|gb|AAC38781.1| delta-orf186 [Staphylococcus aureus]
>gi|3327943|gb|AAC38780.1| multidrug efflux protein QacB [Staphylococcus aureus]
>gi|3327942|gb|AAC38779.1| transcriptional regulator QacR [Staphylococcus aureus]
>gi|3135292|gb|AAC38560.1| large conductance mechanosensitive channel [Staphylococcus aureus]
>gi|3827912|gb|AAC38446.1| IgG-binding protein SBI [Staphylococcus aureus]
>gi|2565311|gb|AAC38087.1| high affinity proline permease [Staphylococcus aureus]
>gi|2315995|gb|AAC38146.1| branched-chain amino acid carrier protein [Staphylococcus aureus]
>gi|4379428|emb|CAA11546.1| thioredoxin reductase [Staphylococcus aureus]
>gi|3445567|gb|AAC32485.1| transport protein [Staphylococcus aureus]
>gi|3445566|gb|AAC32484.1| repressor protein [Staphylococcus aureus]
>gi|3411114|gb|AAC31156.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411112|gb|AAC31155.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411110|gb|AAC31154.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411108|gb|AAC31153.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411106|gb|AAC31152.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411104|gb|AAC31151.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411102|gb|AAC31150.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411100|gb|AAC31149.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411098|gb|AAC31148.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411096|gb|AAC31147.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411092|gb|AAC31144.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411090|gb|AAC31143.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411088|gb|AAC31142.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411086|gb|AAC31141.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411084|gb|AAC31140.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411082|gb|AAC31139.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411080|gb|AAC31138.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411078|gb|AAC31137.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411076|gb|AAC31136.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411074|gb|AAC31135.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|2689564|gb|AAC28969.1| integrase [Staphylococcus aureus]
>gi|2689563|gb|AAC28968.1| enterotoxin [Staphylococcus aureus]
>gi|2689562|gb|AAC28967.1| orf15 [Staphylococcus aureus]
>gi|2689561|gb|AAC28966.1| orf14 [Staphylococcus aureus]
>gi|2689560|gb|AAC28965.1| orf13 [Staphylococcus aureus]
>gi|2689559|gb|AAC28964.1| orf12 [Staphylococcus aureus]
>gi|2689558|gb|AAC28963.1| orf11 [Staphylococcus aureus]
>gi|2689557|gb|AAC28962.1| orf10 [Staphylococcus aureus]
>gi|2689556|gb|AAC28961.1| orf9 [Staphylococcus aureus]
>gi|2689555|gb|AAC28960.1| orf8 [Staphylococcus aureus]
>gi|2689554|gb|AAC28959.1| orf7 [Staphylococcus aureus]
>gi|2689553|gb|AAC28958.1| orf6 [Staphylococcus aureus]
>gi|2689552|gb|AAC28957.1| orf5 [Staphylococcus aureus]
>gi|2689551|gb|AAC28956.1| orf4 [Staphylococcus aureus]

>gi|2689550|gb|AAC28955.1| orf3 [Staphylococcus aureus]
 >gi|2689549|gb|AAC28954.1| toxic shock syndrome toxin-1 [Staphylococcus aureus]
 >gi|2689548|gb|AAC28953.1| orf1 [Staphylococcus aureus]
 >gi|3393011|emb|CAA12115.1| Clumping factor B [Staphylococcus aureus]
 >gi|3323613|gb|AAC26661.1| extracellular enterotoxin type I precursor [Staphylococcus aureus]
 >gi|3323611|gb|AAC26660.1| extracellular enterotoxin type G precursor [Staphylococcus aureus]
 >gi|3256224|emb|CAA74741.1| ypfP [Staphylococcus aureus]
 >gi|3256223|emb|CAA74740.1| UDP-N-acetylmuramyl-tripeptide synthetase [Staphylococcus aureus]
 >gi|3256222|emb|CAA74739.1| peptide chain release factor 3 [Staphylococcus aureus]
 >gi|230814|pdb|3BLM| Beta-Lactamase (E.C.3.5.2.6)
 >gi|230746|pdb|2SNS| Staphylococcal Nuclease (E.C.3.1.33.1) Complex With 2(Prime)-Deoxy-3(Prime)-5(Prime)-Diphosphothymidine
 >gi|230745|pdb|2SNM| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Val 66 Replaced By Lys (V66k)
 >gi|576398|pdb|2ENB| Staphylococcal Nuclease (E.C.3.1.31.1) Mutation With Asp 21 Replaced By Glu (D21e) Complexed With The Inhibitor Thymidine 3',5'-Diphosphate
 >gi|443374|pdb|2DTB| Delta-Toxin (Delta-Haemolysin) (Nmr, 9 Structures)
 >gi|1421454|pdb|1ZER| Mol_id: 1; Molecule: Histidine-Containing Phosphocarrier Protein; Chain: Null; Synonym: Hpr
 >gi|576294|pdb|1SYG| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Ala (P117a)
 >gi|576293|pdb|1SYF| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Thr (P117t) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
 >gi|576292|pdb|1SYE| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Thr (P117t)
 >gi|576291|pdb|1SYD| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Gly (P117g) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
 >gi|576290|pdb|1SYC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Gly (P117g)
 >gi|576289|pdb|1SYB| Staphylococcal Nuclease (E.C.3.1.31.1) With Residues 27 - 31 (Tyr-Lys-Gly-Gln-Pro) Replaced With Residues 160 - 165 Of Concanavalin A (Ser-Ser-Asn-Gly-Ser-Pro) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
 >gi|349914|pdb|1STY| Staphylococcal Nuclease (E.C.3.1.31.1) Insertion Mutant With Glycine Residue Inserted In An Alpha Helix, Between Arg126 And Lys127 (126g127) Complex With Calcium And Inhibitor Thymidine 3',5'-Bisphosphate
 >gi|999674|pdb|1STH| Staphylococcal Nuclease (E.C.3.1.31.1) Complexed With Co(Ii) Ion And Thymidine 3',5'-Bisphosphate (Pdtp)
 >gi|999672|pdb|1STG| Staphylococcal Nuclease (E.C.3.1.31.1)
 >gi|576287|pdb|1STN| Staphylococcal Nuclease (E.C.3.1.31.1)
 >gi|576286|pdb|1STB| Staphylococcal Nuclease (E.C.3.1.31.1) Insertion Mutant With Leu Inserted At The End Of The Third Beta-Strand Between Leu 36 And Leu 37 (Ins(L36-L)) Complexed With Thymidine 3',5'-Diphosphate And Calcium
 >gi|576285|pdb|1STA| Staphylococcal Nuclease (E.C.3.1.31.1) Double Insertion Mutant With Two Glycine Residues Inserted In The First Beta Strand Between Pro 11 And Ala 12 (Ins(P11-Gg)) Complexed With Calcium And The Inhibitor Thymidine 3',5'-Diphosphate
 >gi|230332|pdb|1SNM| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant (Glu 43 Replaced By Asp) (E43D) Complex With A Calcium Ion And 3-Prime, 5-Prime-Deoxythymidine Bisphosphate
 >gi|230331|pdb|1SNC| Staphylococcal Nuclease (E.C.3.1.31.1) Complex With A Calcium Ion And 3-Prime, 5-Prime-Deoxythymidine Bisphosphate
 >gi|1431686|pdb|1PIO|B Chain B, Mol_id: 1; Molecule: Beta-Lactamase; Chain: A, B; Synonym: Penicillinase; Ec: 3.5.2.6; Engineered: Yes; Mutation: Ins(Met 30), A238s, Del(I239)
 >gi|1431685|pdb|1PIO|A Chain A, Mol_id: 1; Molecule: Beta-Lactamase; Chain: A, B; Synonym: Penicillinase; Ec: 3.5.2.6; Engineered: Yes; Mutation: Ins(Met 30), A238s, Del(I239)
 >gi|1127093|pdb|1NSN|S Chain S, Immunoglobulin, Staphylococcal Nuclease Mol_id: 1; Molecule: IgG Fab (IgG1, Kappa); Chain: L, H; Domain: Fragment N10; Synonym: N10 Fab Immunoglobulin; Mol_id: 2; Molecule: Staphylococcal Nuclease; Chain: S; Synonym: Staphylococcal Nuclease Ribonuclease, (Deoxyribonuclease)-3'-Nucleotidohydrolase; Ec: 3.1.31.1; Engineered: Yes
 >gi|999581|pdb|1KDC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Asn (K116n)
 >gi|999578|pdb|1KDB| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Glu (K116e)
 >gi|999577|pdb|1KDA| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Asp (K116d)
 >gi|640137|pdb|1KAN|B Chain B, Kanamycin Nucleotidyltransferase (E.C.2.7.7.-) Mutant With Asp 80 Replaced By Tyr And Thr 130 Replaced By Lys (D80y,T130k)
 >gi|640136|pdb|1KAN|A Chain A, Kanamycin Nucleotidyltransferase (E.C.2.7.7.-) Mutant With Asp 80 Replaced By Tyr And Thr 130 Replaced By Lys (D80y,T130k)
 >gi|494228|pdb|1KAB| Staphylococcal Nuclease (E.C.3.1.33.1) Mutant With Lys 116 Replaced By Gly (K116g)
 >gi|494227|pdb|1KAA| Staphylococcal Nuclease (E.C.3.1.33.1) Mutant With Lys 116 Replaced By Ala (K116a)

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>gi|229907|pdb|1FC2|C Chain C, Immunoglobulin Fc And Fragment B Of Protein A Complex
>gi|576100|pdb|1ENC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Asp 21 Replaced By Glu
(D21e) Complexed With A Calcium Ion And The Inhibitor Thymidine 3',5'-Diphosphate
>gi|576099|pdb|1ENA| Staphylococcal Nuclease (E.C.3.1.31.1) Mutation With Asp 21 Replaced By Glu
(D21e) Complexed With A Calcium Ion
>gi|442844|pdb|1DTC| Acetyl-Delta-Toxin (Acetyl-Delta-Haemolysin) (Nmr, 12 Structures)
>gi|640251|pdb|1BLH| Beta-Lactamase (E.C.3.5.2.6) Complexed With [[n-
(Benzyloxycarbonyl)amino]methyl]phosphonate
>gi|515092|pdb|1BLP| Beta-Lactamase (E.C.3.5.2.6) P54 Mutant With Asp 179 Replaced By Asn (D179n)
>gi|493890|pdb|1BLC| Beta-Lactamase (E.C.3.5.2.6) Complex With Degradation Products Of Clavulanate
>gi|3152725|gb|AAC17130.1| enolase [Staphylococcus aureus]
>gi|2463563|dbj|BAA22556.1| MURD [Staphylococcus aureus]
>gi|2463562|dbj|BAA22555.1| MRAY [Staphylococcus aureus]
>gi|2463561|dbj|BAA22554.1| penicillin-binding protein 1 [Staphylococcus aureus]
>gi|2463560|dbj|BAA22553.1| unnamed protein product [Staphylococcus aureus]
>gi|2463559|dbj|BAA22552.1| unnamed protein product [Staphylococcus aureus]
>gi|1835218|emb|CAA71057.1| seryl-trna synthetase [Staphylococcus aureus]
>gi|3122772|sp|O31203|RRF1_STAAU PROBABLE RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR)
(RRF)
>gi|1488695|gb|AAC12901.1| novel antigen; orf-2 [Staphylococcus aureus]
>gi|2826896|dbj|BAA24572.1| RecG [Staphylococcus aureus]
>gi|2791991|emb|CAA74380.1| putative transposase [Staphylococcus aureus]
>gi|2791990|emb|CAA74379.1| hypothetical protein [Staphylococcus aureus]
>gi|2791989|emb|CAA74378.1| hypothetical protein [Staphylococcus aureus]
>gi|2791988|emb|CAA74377.1| hypothetical protein [Staphylococcus aureus]
>gi|2791987|emb|CAA74376.1| PBP2A [Staphylococcus aureus]
>gi|2791986|emb|CAA74375.1| MecR1 protein [Staphylococcus aureus]
>gi|2791985|emb|CAA74374.1| MecI protein [Staphylococcus aureus]
>gi|2791984|emb|CAA74373.1| putative repressor [Staphylococcus aureus]
>gi|2769708|gb|AAB95639.1| pristinamycin resistance protein VgaB [Staphylococcus aureus]
>gi|2736228|gb|AAB94106.1| transducer protein [Staphylococcus aureus]
>gi|2736227|gb|AAB94105.1| mutant sensor protein [Staphylococcus aureus]
>gi|2736226|gb|AAB94104.1| pre-pheromone [Staphylococcus aureus]
>gi|2736225|gb|AAB94103.1| signal transduction protein [Staphylococcus aureus]
>gi|2736223|gb|AAB94102.1| transducer protein [Staphylococcus aureus]
>gi|2736222|gb|AAB94101.1| mutant sensor protein [Staphylococcus aureus]
>gi|2736221|gb|AAB94100.1| pre-pheromone [Staphylococcus aureus]
>gi|2736220|gb|AAB94099.1| signal transduction protein [Staphylococcus aureus]
>gi|2736218|gb|AAB94098.1| transducer protein [Staphylococcus aureus]
>gi|2736217|gb|AAB94097.1| mutant sensor protein [Staphylococcus aureus]
>gi|2736216|gb|AAB94096.1| pre-pheromone [Staphylococcus aureus]
>gi|2736215|gb|AAB94095.1| signal transduction protein [Staphylococcus aureus]
>gi|2696796|dbj|BAA24012.1| Fmt [Staphylococcus aureus]
>gi|2696713|dbj|BAA24009.1| integrase [Staphylococcus aureus]
>gi|2696712|dbj|BAA24008.1| LukF-PV [Staphylococcus aureus]
>gi|2696711|dbj|BAA24007.1| LukS-PV [Staphylococcus aureus]
>gi|216977|dbj|BAA00126.1| staphylocoagulase precursor [Staphylococcus aureus]
>gi|773396|emb|CAA39963.1| QacA protein [Staphylococcus aureus]
>gi|46660|emb|CAA39962.1| ORF188, has identity with known regulators such as tet regulator in Tn10
[Staphylococcus aureus]
>gi|2645713|gb|AAB87473.1| ribosome recycling factor [Staphylococcus aureus]
>gi|2641998|dbj|BAA23610.1| lipophilic protein [Staphylococcus aureus]
>gi|2580436|dbj|BAA23141.1| histidyl-tRNA synthetase [Staphylococcus aureus]
>gi|2580435|dbj|BAA23140.1| N-acetylmuramoyl-L-alanine amidase [Staphylococcus aureus]
>gi|2580434|dbj|BAA23139.1| ORF1 [Staphylococcus aureus]
>gi|2580433|dbj|BAA23138.1| ppGpp hydrolase [Staphylococcus aureus]
>gi|2580432|dbj|BAA23137.1| adenine phosphoribosyltransferase [Staphylococcus aureus]
>gi|1575062|gb|AAB81288.1| lytS [Staphylococcus aureus]
>gi|1575061|gb|AAB81287.1| ScdA [Staphylococcus aureus]
>gi|1694677|dbj|BAA13755.1| DnaA [Staphylococcus aureus]
>gi|2506163|gb|AAB81232.1| AgrD [Staphylococcus aureus]
>gi|1916240|gb|AAB81231.1| AgrA [Staphylococcus aureus]
>gi|1916239|gb|AAB81230.1| AgrC-31 [Staphylococcus aureus]
>gi|1916238|gb|AAB81229.1| AgrB [Staphylococcus aureus]
>gi|2506165|gb|AAB80783.1| AgrD [Staphylococcus aureus]
>gi|2506164|gb|AAB80779.1| AgrD [Staphylococcus aureus]
>gi|1916248|gb|AAB80782.1| AgrA [Staphylococcus aureus]
>gi|1916247|gb|AAB80781.1| AgrC [Staphylococcus aureus]
>gi|1916246|gb|AAB80780.1| AgrB [Staphylococcus aureus]
>gi|1916244|gb|AAB80778.1| AgrA [Staphylococcus aureus]
>gi|1916243|gb|AAB80777.1| AgrC [Staphylococcus aureus]

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>gi|1916242|gb|AAB80776.1| AgrB [Staphylococcus aureus]
 >gi|2344765|dbj|BAA21889.1| glutamic acid-specific protease [Staphylococcus aureus]
 >gi|2302281|emb|CAA03107.1| unnamed protein product [Staphylococcus aureus]
 >gi|2302279|emb|CAA03106.1| unnamed protein product [Staphylococcus aureus]
 >gi|2258300|gb|AAB63269.1| AgrC [Staphylococcus aureus]
 >gi|2258299|gb|AAB63268.1| AgrD [Staphylococcus aureus]
 >gi|2258298|gb|AAB63267.1| AgrB [Staphylococcus aureus]
 >gi|2258296|gb|AAB63266.1| AgrC [Staphylococcus aureus]
 >gi|2258295|gb|AAB63265.1| AgrD [Staphylococcus aureus]
 >gi|2258294|gb|AAB63264.1| AgrB [Staphylococcus aureus]
 >gi|2239274|gb|AAB62278.1| peptidoglycan hydrolase [Staphylococcus aureus]
 >gi|2224842|emb|CAA52098.1| squalene synthase [Staphylococcus aureus]
 >gi|2224841|emb|CAA52097.1| squalene desaturase [Staphylococcus aureus]
 >gi|437916|emb|CAA52296.1| isoleucyl-tRNA synthetase [Staphylococcus aureus]
 >gi|2190507|emb|CAA71446.1| outer surface binding 70kD protein [Staphylococcus aureus]
 >gi|153069|gb|AAB59090.1| sigma factor
 >gi|4433370|dbj|BAA22521.1| lipophilic protein which affects bacterial lysis rate and methicillin resistance level [Staphylococcus aureus]
 >gi|1262748|dbj|BAA12148.1| LukF-PV like component [Staphylococcus aureus]
 >gi|1230554|dbj|BAA12147.1| LukM component [Staphylococcus aureus]
 >gi|725454|dbj|BAA04185.1| autolysin [Staphylococcus aureus]
 >gi|725453|dbj|BAA04184.1| ORF3 [Staphylococcus aureus]
 >gi|725452|dbj|BAA04183.1| ORF2 [Staphylococcus aureus]
 >gi|725451|dbj|BAA04182.1| ORF1 [Staphylococcus aureus]
 >gi|540542|dbj|BAA01370.1| DNA gyrase A [Staphylococcus aureus]
 >gi|540541|dbj|BAA01369.1| DNA gyrase B [Staphylococcus aureus]
 >gi|522106|dbj|BAA06360.1| HSP40 [Staphylococcus aureus]
 >gi|487331|dbj|BAA06361.1| ORF35 [Staphylococcus aureus]
 >gi|487327|dbj|BAA06357.1| ORF37 [Staphylococcus aureus]
 >gi|441211|dbj|BAA06359.1| HSP70 [Staphylococcus aureus]
 >gi|441210|dbj|BAA06358.1| HSP20 [Staphylococcus aureus]
 >gi|441208|dbj|BAA03533.1| HSP60 [Staphylococcus aureus]
 >gi|441207|dbj|BAA03532.1| HSP10 [Staphylococcus aureus]
 >gi|216975|dbj|BAA14147.1| ORF for norA [Staphylococcus aureus]
 >gi|1483182|dbj|BAA13160.1| DNA polymerase III [Staphylococcus aureus]
 >gi|1777321|dbj|BAA11087.1| DNA topoisomerase IV GrlA subunit [Staphylococcus aureus]
 >gi|1777320|dbj|BAA11086.1| DNA topoisomerase IV GrlB subunit [Staphylococcus aureus]
 >gi|1777318|dbj|BAA11085.1| DNA topoisomerase IV GrlA subunit [Staphylococcus aureus]
 >gi|1777317|dbj|BAA11084.1| DNA topoisomerase IV GrlB subunit [Staphylococcus aureus]
 >gi|628920|pir||S40421 hypothetical protein - Staphylococcus aureus
 >gi|97848|pir||S12902 ricin chain A - Staphylococcus aureus
 >gi|97853|pir||S14180 transposase - Staphylococcus aureus (fragment)
 >gi|79909|pir||JU0116 transposase (insertion sequence IS431) - Staphylococcus aureus
 >gi|79889|pir||S00092 penicillin-binding protein - Staphylococcus aureus
 >gi|79872|pir||S04360 lacB protein - Staphylococcus aureus (fragment)
 >gi|628921|pir||S40422 hypothetical protein - Staphylococcus aureus
 >gi|1084186|pir||S54707 dnaA protein - Staphylococcus aureus
 >gi|628917|pir||S27240 enterotoxin B - Staphylococcus aureus (fragments)
 >gi|79852|pir||A29566 enterotoxin A - Staphylococcus aureus
 >gi|79850|pir||S02008 dihydrofolate reductase (EC 1.5.1.3) - Staphylococcus aureus (fragment)
 >gi|79845|pir||S15766 beta-hemolysin - Staphylococcus aureus
 >gi|97845|pir||C42295 recf protein - Staphylococcus aureus (fragment)
 >gi|2078390|gb|AAB54024.1| SecA [Staphylococcus aureus]
 >gi|2078382|gb|AAB54022.1| SecY [Staphylococcus aureus]
 >gi|2078381|gb|AAB54021.1| ribosomal protein L15 [Staphylococcus aureus]
 >gi|2078380|gb|AAB54020.1| ribosomal protein L30 [Staphylococcus aureus]
 >gi|2078378|gb|AAB54019.1| RplK; ribosomal protein L11 [Staphylococcus aureus]
 >gi|2078377|gb|AAB54018.1| NusG [Staphylococcus aureus]
 >gi|2078376|gb|AAB54017.1| SecE [Staphylococcus aureus]
 >gi|2058356|emb|CAB06539.1| dihydropterolate synthase [Staphylococcus aureus]
 >gi|1943995|dbj|BAA19494.1| sigA=sigma70 [Staphylococcus aureus]
 >gi|1943994|dbj|BAA19493.1| dnaG [Staphylococcus aureus]
 >gi|1943993|dbj|BAA19492.1| orf30 [Staphylococcus aureus]
 >gi|1943992|dbj|BAA19491.1| orf15 [Staphylococcus aureus]
 >gi|1934992|emb|CAA68933.1| ORF6 [Staphylococcus aureus]
 >gi|1934991|emb|CAA68932.1| sigma factor B [Staphylococcus aureus]
 >gi|1934990|emb|CAA68931.1| rsbW [Staphylococcus aureus]
 >gi|1934989|emb|CAA68930.1| rsbV [Staphylococcus aureus]
 >gi|1934988|emb|CAA68929.1| rsbU [Staphylococcus aureus]
 >gi|1934987|emb|CAA68928.1| ORF1 [Staphylococcus aureus]
 >gi|1916317|gb|AAB51152.1| alkyl hydroperoxide reductase subunit F [Staphylococcus aureus]

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>gi|1916316|gb|AAB51151.1| alkyl hydroperoxide reductase subunit C [Staphylococcus aureus]
>gi|1913907|gb|AAB51063.1| TagD [Staphylococcus aureus]
>gi|1913906|gb|AAB51062.1| TagX [Staphylococcus aureus]
>gi|1913905|gb|AAB51061.1| TagB [Staphylococcus aureus]
>gi|1864022|gb|AAB50178.1| penicillin binding protein 4
>gi|881631|gb|AAB50179.1| AbcA
>gi|1657655|gb|AAB49445.1| Cap8P [Staphylococcus aureus]
>gi|1657654|gb|AAB49444.1| Cap8O [Staphylococcus aureus]
>gi|1657653|gb|AAB49443.1| Cap8N [Staphylococcus aureus]
>gi|1657652|gb|AAB49442.1| Cap8M [Staphylococcus aureus]
>gi|1657651|gb|AAB49441.1| Cap8L [Staphylococcus aureus]
>gi|1657650|gb|AAB49440.1| Cap8K [Staphylococcus aureus]
>gi|1657649|gb|AAB49439.1| Cap8J [Staphylococcus aureus]
>gi|1657648|gb|AAB49438.1| Cap8I [Staphylococcus aureus]
>gi|1657647|gb|AAB49437.1| Cap8H [Staphylococcus aureus]
>gi|1657646|gb|AAB49436.1| Cap8G [Staphylococcus aureus]
>gi|1657645|gb|AAB49435.1| Cap8F [Staphylococcus aureus]
>gi|1657644|gb|AAB49434.1| Cap8E [Staphylococcus aureus]
>gi|1657643|gb|AAB49433.1| Cap8D [Staphylococcus aureus]
>gi|1657642|gb|AAB49432.1| Cap8C [Staphylococcus aureus]
>gi|1657641|gb|AAB49431.1| Cap8B [Staphylococcus aureus]
>gi|1657640|gb|AAB49430.1| Cap8A [Staphylococcus aureus]
>gi|1854577|gb|AAB48183.1| lytR [Staphylococcus aureus]
>gi|862312|gb|AAB48182.1| lytS [Staphylococcus aureus]
>gi|1731452|gb|AAB48104.1| recombination protein [Staphylococcus aureus]
>gi|1053003|gb|AAB48103.1| CAT protein [Staphylococcus aureus]
>gi|1053002|gb|AAB48102.1| replication protein [Staphylococcus aureus]
>gi|1848269|gb|AAB47993.1| quaternary ammonium compounds resistance protein Qac [Staphylococcus aureus]
>gi|1848268|gb|AAB47992.1| replication protein Rep [Staphylococcus aureus]
>gi|677847|emb|CAA24593.1| reading frame A [Staphylococcus aureus]
>gi|677846|emb|CAA24590.1| reading frame C [Staphylococcus aureus]
>gi|677845|emb|CAA24589.1| reading frame D [Staphylococcus aureus]
>gi|677844|emb|CAA24588.1| reading frame E [Staphylococcus aureus]
>gi|46746|emb|CAA38969.1| truncated alpha-toxin [Staphylococcus aureus]
>gi|46559|emb|CAA24592.1| reading frame F transl. attenuator [Staphylococcus aureus]
>gi|46558|emb|CAA24591.1| reading frame B mls resistance [Staphylococcus aureus]
>gi|987499|gb|AAB41908.1| 5-dehydroquinase synthase
>gi|987498|gb|AAB41907.1| chorismate synthase
>gi|987497|gb|AAB41906.1| nucleoside diphosphate kinase
>gi|987496|gb|AAB41905.1| geranylgeranyl pyrophosphate synthetase homolog; Method: conceptual translation supplied by author
>gi|1262138|emb|CAA62900.1| glycerol 3-phosphate cytidyltransferase [Staphylococcus aureus]
>gi|1262137|emb|CAA62899.1| penicillin-binding protein 4 [Staphylococcus aureus]
>gi|1262136|emb|CAA62898.1| ATP-binding cassette transporter A [Staphylococcus aureus]
>gi|1045529|gb|AAB39957.1| beta-lactamase
>gi|1045527|gb|AAB39956.1| beta-lactamase
>gi|1045525|gb|AAB39955.1| tetracycline resistance protein [Staphylococcus aureus]
>gi|1045524|gb|AAB39954.1| replication protein [Staphylococcus aureus]
>gi|1684749|emb|CAA70762.1| femD [Staphylococcus aureus]
>gi|1204146|emb|CAA65106.1| fibronectin-binding protein [Staphylococcus aureus]
>gi|1684751|emb|CAA70579.1| DNA directed RNA polymerase beta' chain [Staphylococcus aureus]
>gi|1478385|gb|AAB36169.1| MsrSa=63 kda MsrA homolog (N-terminal) [Staphylococcus aureus, clinical isolate, pEP2104, Peptide Plasmid Partial, 31 aa]
>gi|1042046|gb|AAB34958.1| IgG-binding polypeptide=protein A homolog [Staphylococcus aureus, strain 8325-4, Peptide Partial, 84 aa]
>gi|999313|gb|AAB34910.1| 60 kda vitronectin-binding surface protein (N-terminal) [Staphylococcus aureus, prototype V8, Peptide Partial, 20 aa]
>gi|998765|gb|AAB34258.1| enterotoxin H (N-terminal) [Staphylococcus aureus, FRI-569, Peptide Partial, 30 aa]
>gi|894289|gb|AAB33482.1| alkaline shock protein 23, ASP23 [Staphylococcus aureus, 912, Peptide, 169 aa]
>gi|619317|gb|AAB32218.1| beta-hemolysin, phospholipase C, PLC [Staphylococcus aureus, 126/89, Peptide, 331 aa]
>gi|693735|gb|AAB31949.1| NorA {ISP794, quinolone resistance} [Staphylococcus aureus, NCTC 8325, Peptide Insertion, 388 aa]
>gi|456770|gb|AAB28795.1| Tet(K)=tetracycline efflux protein [Staphylococcus aureus, pT181, Peptide Plasmid, 459 aa]
>gi|433036|gb|AAB28599.1| adhesin (collagen binding domain) [Staphylococcus aureus, FDA 574, Peptide Partial, 37 aa]
>gi|1680566|gb|AH004229.1| No definition line found
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>gi|1680565|gb|AH004228.1| No definition line found
>gi|299115|gb|AAB26122.1| gamma-hemolysin component II, H gamma II=leukocidin S homolog
[Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 5 aa, segment 2 of 2]
>gi|299114|gb|AAB26121.1| gamma-hemolysin component II, H gamma II=leukocidin S homolog
[Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 58 aa, segment 1 of 2]
>gi|299112|gb|AAB26120.1| gamma-hemolysin component I, H gamma I=leukocidin F homolog
[Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 2 aa, segment 2 of 2]
>gi|299111|gb|AAB26119.1| gamma-hemolysin component I, H gamma I=leukocidin F homolog
[Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 59 aa, segment 1 of 2]
>gi|265412|gb|AAB25337.1| V8 protease [Staphylococcus aureus, Peptide, 276 aa]
>gi|248665|gb|AAB22051.1| chloramphenicol acetyltransferase, CAT [EC 2.3.1.28] [Staphylococcus
aureus, 4.6 kb chloramphenicol resistance (CmR) plasmid pSCS6, Peptide Plasmid, 215 aa]
>gi|246440|gb|AAB21603.1| 60 kda cell surface adhesin for heparan sulfate [Staphylococcus aureus,
Peptide Partial, 4 aa]
>gi|246439|gb|AAB21602.1| 66 kda cell surface adhesin for heparan sulfate [Staphylococcus aureus,
Peptide Partial, 9 aa]
>gi|239960|gb|AAB20545.1| 25-kda elastin-binding protein [Staphylococcus aureus, Peptide Partial, 14
aa]
>gi|239959|gb|AAB20544.1| 40-kda elastin-binding protein [Staphylococcus aureus, Peptide Partial, 18
aa]
>gi|1673527|gb|AAB18959.1| transposase [Staphylococcus aureus]
>gi|1673525|gb|AAB18958.1| transposase [Staphylococcus aureus]
>gi|1644433|gb|AAB17663.1| D-specific D-2-hydroxyacid dehydrogenase [Staphylococcus aureus]
>gi|581567|emb|CAA37260.1| Sau96I DNA methyltransferase [Staphylococcus aureus]
>gi|46618|emb|CAA37259.1| Sau96I restriction endonuclease [Staphylococcus aureus]
>gi|46597|emb|CAA37902.1| transposase [Staphylococcus aureus]
>gi|1587088|prf|2205353A pheromone [Staphylococcus aureus]
>gi|1583755|prf|12121375A MHC class II-like protein [Staphylococcus aureus]
>gi|229342|prf|710414A nuclease [Staphylococcus aureus]
>gi|229233|prf|670719A nuclease [Staphylococcus aureus]
>gi|1096955|prf|2113202C RNA polymerase:SUBUNIT=beta' [Staphylococcus aureus]
>gi|1096954|prf|2113202B RNA polymerase:SUBUNIT=beta [Staphylococcus aureus]
>gi|1096953|prf|2113202A ORF 202 [Staphylococcus aureus]
>gi|1095875|prf|2110238A lipase [Staphylococcus aureus]
>gi|1094971|prf|2107219C RNA polymerase:SUBUNIT=beta' [Staphylococcus aureus]
>gi|1094970|prf|2107219B RNA polymerase:SUBUNIT=beta [Staphylococcus aureus]
>gi|1094969|prf|2107219A rpoB upstream ORF [Staphylococcus aureus]
>gi|1093504|prf|2104216A LukM protein [Staphylococcus aureus]
>gi|1092377|prf|2023311A exotoxin [Staphylococcus aureus]
>gi|742313|prf|2009360B pcrB protein [Staphylococcus aureus]
>gi|742312|prf|2009360A helicase [Staphylococcus aureus]
>gi|448909|prf|1918210C leukocidin [Staphylococcus aureus]
>gi|448908|prf|1918210B leukocidin [Staphylococcus aureus]
>gi|448907|prf|1918210A gamma hemolysin [Staphylococcus aureus]
>gi|444424|prf|1907159A ethidium bromide resistance gene [Staphylococcus aureus]
>gi|384172|prf|1905282A rep protein [Staphylococcus aureus]
>gi|384170|prf|1905280A protein A [Staphylococcus aureus]
>gi|383540|prf|1903261A toxic shock syndrome toxin [Staphylococcus aureus]
>gi|228896|prf|1814271A Glu-C endoprotease [Staphylococcus aureus]
>gi|228567|prf|1806229B repressor [Staphylococcus aureus]
>gi|228566|prf|1806229A coinducer protein [Staphylococcus aureus]
>gi|228100|prf|1717222A REP protein [Staphylococcus aureus]
>gi|227968|prf|1714238A beta lactamase mutant S-3P [Staphylococcus aureus]
>gi|227467|prf|1704203A enterotoxin A [Staphylococcus aureus]
>gi|226860|prf|1609133A plasmid pOX1000 ORF A [Staphylococcus aureus]
>gi|581544|emb|CAA27142.1| kanamycin nucleotidyltransferase (AA 1-253) [Staphylococcus aureus]
>gi|46496|emb|CAA27141.1| repB polypeptide (AA 1-235) [Staphylococcus aureus]
>gi|1245474|gb|AAB09712.1| nicking enzyme [Staphylococcus aureus]
>gi|1586531|prf|2204232B penicillin-binding protein 4 [Staphylococcus aureus]
>gi|1586530|prf|2204232A ABC transporter-like protein [Staphylococcus aureus]
>gi|1585878|prf|2202209C ORF 3 [Staphylococcus aureus]
>gi|1585877|prf|2202209B ORF 2 [Staphylococcus aureus]
>gi|1585876|prf|2202209A ORF 1 [Staphylococcus aureus]
>gi|1053140|gb|AAB09660.1| tetracycline resistance protein [Staphylococcus aureus]
>gi|1575125|gb|AAB09464.1| beta-lactamase
>gi|226340|prf|1507213A transposase, insertion seq IS257 [Staphylococcus aureus]
>gi|225999|prf|1405331D repE gene [Staphylococcus aureus]
>gi|225998|prf|1405331C ORF D [Staphylococcus aureus]
>gi|225997|prf|1405331B rlx gene [Staphylococcus aureus]
>gi|359739|prf|1313299A staphylocoagulase [Staphylococcus aureus]
>gi|225442|prf|1303274B gene B [Staphylococcus aureus]

>gi|224810|prf||1202257F ORF [Staphylococcus aureus]
 >gi|224809|prf||1202257E gene tnpC [Staphylococcus aureus]
 >gi|224808|prf||1202257D gene tnpB [Staphylococcus aureus]
 >gi|224806|prf||1202257B gene spc [Staphylococcus aureus]
 >gi|224805|prf||1202257A gene ermA [Staphylococcus aureus]
 >gi|1567208|emb|CAA02065.1| Ble [Staphylococcus aureus]
 >gi|860732|gb|AAB07805.1| phosphoenolpyruvate carboxykinase [Staphylococcus aureus]
 >gi|1272327|gb|AAB07765.1| 3'5'-aminoglycoside phosphotransferase [Staphylococcus aureus]
 >gi|1272326|gb|AAB07764.1| truncated streptothricin acetyl transferase [Staphylococcus aureus]
 >gi|1236640|gb|AAB07747.1| multidrug resistance protein [Staphylococcus aureus]
 >gi|1236639|gb|AAB07746.1| partial duplication of the qacC gene [Staphylococcus aureus]
 >gi|1236638|gb|AAB07745.1| replication protein [Staphylococcus aureus]
 >gi|1053000|gb|AAB07714.1| replication protein [Staphylococcus aureus]
 >gi|1052999|gb|AAB07713.1| recombination protein [Staphylococcus aureus]
 >gi|1052998|gb|AAB07712.1| tetracycline resistance protein [Staphylococcus aureus]
 >gi|1125687|emb|CAA60583.1| glycerol-3-phosphate cytidyltransferase [Staphylococcus aureus]
 >gi|1125686|emb|CAA60582.1| penicillin binding protein 4 [Staphylococcus aureus]
 >gi|1125685|emb|CAA60581.1| mdr [Staphylococcus aureus]
 >gi|1125683|emb|CAA60586.1| glycerol-3-phosphate cytidyltransferase [Staphylococcus aureus]
 >gi|1125682|emb|CAA60585.1| penicillin binding protein 4 [Staphylococcus aureus]
 >gi|1125681|emb|CAA60584.1| mdr [Staphylococcus aureus]
 >gi|1495791|emb|CAA61517.1| DNA-directed RNA polymerase [Staphylococcus aureus]
 >gi|758691|gb|AAB06195.1| enterotoxin D
 >gi|1480567|gb|AAB05743.1| protein A
 >gi|1477533|gb|AAB05396.1| sarA
 >gi|1477532|gb|AAB05395.1| ORF3
 >gi|225996|prf||1405331A str gene [Staphylococcus aureus]
 >gi|225995|prf||1405330A repM gene [Staphylococcus aureus]
 >gi|225821|prf||1314205A protein A [Staphylococcus aureus]
 >gi|225444|prf||1303274D gene D [Staphylococcus aureus]
 >gi|225443|prf||1303274C gene C [Staphylococcus aureus]
 >gi|225441|prf||1303274A gene A [Staphylococcus aureus]
 >gi|224812|prf||1202257H peptide 2 [Staphylococcus aureus]
 >gi|224811|prf||1202257G peptide 1 [Staphylococcus aureus]
 >gi|224807|prf||1202257C gene tnpA [Staphylococcus aureus]
 >gi|224650|prf||1109959A nuclease, staphylococcal [Staphylococcus aureus]
 >gi|223937|prf||1005204A hemolysin delta [Staphylococcus aureus]
 >gi|1408063|gb|AAB03636.1| methicillin-resistance protein
 >gi|295162|gb|AAB03637.1| unknown ORF1; putative
 >gi|1407784|gb|AAB03613.1| orf-1; novel antigen
 >gi|642270|emb|CAA88043.1| DNA polymerase III [Staphylococcus aureus]
 >gi|1311537|gb|AAB02113.1| cop protein
 >gi|153094|gb|AAB02114.1| resistance protein
 >gi|153092|gb|AAB02112.1| replication protein
 >gi|673492|emb|CAA24594.1| nuclease [Staphylococcus aureus]
 >gi|1340131|emb|CAA66627.1| ORF4 [Staphylococcus aureus]
 >gi|1340130|emb|CAA66626.1| ORF3 [Staphylococcus aureus]
 >gi|1340129|emb|CAA66625.1| ORF2 [Staphylococcus aureus]
 >gi|1340128|emb|CAA66624.1| ORF1 [Staphylococcus aureus]
 >gi|758303|emb|CAA24957.1| staphylokinase [Staphylococcus aureus]
 >gi|736295|emb|CAA27035.1| A protein [Staphylococcus aureus]
 >gi|581591|emb|CAA34491.1| beta-lactamase (AA 1-281) [Staphylococcus aureus]
 >gi|581590|emb|CAA36953.1| blaZ protein (AA 1-281) [Staphylococcus aureus]
 >gi|581589|emb|CAA36950.1| binL protein (AA 1-197) [Staphylococcus aureus]
 >gi|46765|emb|CAA25801.1| put. alpha-toxin precursor (aa -26 to 293) [Staphylococcus aureus]
 >gi|46759|emb|CAA36952.1| blaR1 protein (AA 1-585) [Staphylococcus aureus]
 >gi|46758|emb|CAA36951.1| blaI protein (AA 1-126) [Staphylococcus aureus]
 >gi|46756|emb|CAA36949.1| ORF480 (pot. transposase) (AA 1-480) [Staphylococcus aureus]
 >gi|46755|emb|CAA36948.1| ORF271 (pot. ATP-binding protein) (AA 1-271) [Staphylococcus aureus]
 >gi|46753|emb|CAA31652.1| transposase (AA 1-224) [Staphylococcus aureus]
 >gi|46752|emb|CAA31651.1| transposase (AA 1-224) [Staphylococcus aureus]
 >gi|46751|emb|CAA31650.1| ORF140 (AA 1-140) [Staphylococcus aureus]
 >gi|46750|emb|CAA31649.1| S1 DHFR (AA 1-161) [Staphylococcus aureus]
 >gi|46749|emb|CAA31648.1| thymidylate synthetase (AA 1-318) [Staphylococcus aureus]
 >gi|46748|emb|CAA31647.1| transposase (AA 1-224) [Staphylococcus aureus]
 >gi|758275|emb|CAA29822.1| sak42D staphylokinase [Staphylococcus aureus]
 >gi|581583|emb|CAA24596.1| protein A [Staphylococcus aureus]
 >gi|459257|emb|CAA83066.1| Potential membrane spanning protein [Staphylococcus aureus]
 >gi|459256|emb|CAA83065.1| Potential ABC transporter [Staphylococcus aureus]
 >gi|46737|emb|CAA34476.1| precursor polypeptide (AA -26 to 632) [Staphylococcus aureus]
 >gi|46691|emb|CAA43604.1| protein A [Staphylococcus aureus]

>gi|46687|emb|CAA68434.1| preproenzyme (AA -68 to 268) [Staphylococcus aureus]
>gi|1070386|emb|CAA63689.1| phosphoenolpyruvate-protein phosphatase [Staphylococcus aureus]
>gi|1070385|emb|CAA63688.1| histidin-containing protein [Staphylococcus aureus]
>gi|677852|emb|CAA45513.1| DNA-directed RNA polymerase beta' chain [Staphylococcus aureus]
>gi|677851|emb|CAA45512.1| DNA-directed RNA polymerase beta chain [Staphylococcus aureus]
>gi|677850|emb|CAA45511.1| hypothetical protein [Staphylococcus aureus]
>gi|677849|emb|CAA45510.1| ribosomal protein L7/L12 [Staphylococcus aureus]
>gi|581571|emb|CAA43217.1| chlorAMPhenicol acetyltransferase [Staphylococcus aureus]
>gi|551670|emb|CAA51251.1| lukS [Staphylococcus aureus]
>gi|551669|emb|CAA51250.1| ORF [Staphylococcus aureus]
>gi|288292|emb|CAA51252.1| leucocidin F [Staphylococcus aureus]
>gi|46652|emb|CAA43218.1| chlorAMPhenicol acetyltransferase [Staphylococcus aureus]
>gi|1333818|emb|CAA26369.1| pot. orfB (aa 1-92) (4557 is 2nd base in codon) [Staphylococcus aureus]
>gi|1333817|emb|CAA26368.1| pot. orfA [Staphylococcus aureus]
>gi|809754|emb|CAA26365.1| unidentified reading frame [Staphylococcus aureus]
>gi|581570|emb|CAA41339.1| dihydrolipoamide acetyltransferase: subunit E2 [Staphylococcus aureus]
>gi|581568|emb|CAA27733.1| beta-lactamase (aa 1-281) [Staphylococcus aureus]
>gi|488529|emb|CAA45728.1| S component of leucocodin R [Staphylococcus aureus]
>gi|483534|emb|CAA44177.1| penicillin-binding protein 2 [Staphylococcus aureus]
>gi|295834|emb|CAA39320.1| ORF 154 [Staphylococcus aureus]
>gi|48874|emb|CAA41340.1| dihydrolipoamide dehydrogenase: subunit E3 [Staphylococcus aureus]
>gi|48872|emb|CAA41338.1| pyruvate dehydrogenase (lipoamide): subunit E1beta [Staphylococcus aureus]
>gi|46647|emb|CAA29842.1| ORF (repE) [Staphylococcus aureus]
>gi|46646|emb|CAA29841.1| orfD [Staphylococcus aureus]
>gi|46645|emb|CAA29840.1| ORF (rlx) [Staphylococcus aureus]
>gi|46644|emb|CAA29839.1| ORF (str) [Staphylococcus aureus]
>gi|46639|emb|CAA31314.1| ORF 1 (AA 1 - 330) [Staphylococcus aureus]
>gi|46638|emb|CAA31313.1| ORF 2 (AA 1 - 236) [Staphylococcus aureus]
>gi|46636|emb|CAA30291.1| RepM protein (AA 1 - 314) [Staphylococcus aureus]
>gi|46632|emb|CAA26367.1| CAT gene (aa 1-215) [Staphylococcus aureus]
>gi|46631|emb|CAA26366.1| repD (aa 1-311) [Staphylococcus aureus]
>gi|46629|emb|CAA68684.1| penicillin-binding protein (AA 1-670) [Staphylococcus aureus]
>gi|46622|emb|CAA42079.1| E.coli isoleucyl tRNA synthetase homologue [Staphylococcus aureus]
>gi|46620|emb|CAA42080.1| E.coli isoleucyl tRNA synthetase homologue [Staphylococcus aureus]
>gi|46611|emb|CAA36829.1| BBP2' (AA 1-668) [Staphylococcus aureus]
>gi|46609|emb|CAA45729.1| F component of leucocodin R [Staphylococcus aureus]
>gi|1134886|emb|CAA54030.1| glutamine synthetase [Staphylococcus aureus]
>gi|581562|emb|CAA44726.1| fibronectin binding protein B [Staphylococcus aureus]
>gi|550424|emb|CAA57278.1| hlgB-like ORF [Staphylococcus aureus]
>gi|550423|emb|CAA57277.1| hlgC-like ORF [Staphylococcus aureus]
>gi|550422|emb|CAA57276.1| hlgA-like ORF [Staphylococcus aureus]
>gi|468509|emb|CAA54029.1| glutamine synthetase repressor [Staphylococcus aureus]
>gi|468508|emb|CAA54028.1| ORF1 [Staphylococcus aureus]
>gi|311976|emb|CAA50893.1| fibrinogen-binding protein [Staphylococcus aureus]
>gi|311974|emb|CAA50892.1| fibrinogen-binding protein [Staphylococcus aureus]
>gi|296396|emb|CAA50571.1| DNA gyrase [Staphylococcus aureus]
>gi|296395|emb|CAA50570.1| DNA gyrase [Staphylococcus aureus]
>gi|296394|emb|CAA50569.1| RecF [Staphylococcus aureus]
>gi|48713|emb|CAA36830.1| orf145 [Staphylococcus aureus]
>gi|46606|emb|CAA32936.1| lacD polypeptide (AA 1-326) [Staphylococcus aureus]
>gi|46605|emb|CAA32935.1| lacC polypeptide (AA 1-310) [Staphylococcus aureus]
>gi|46589|emb|CAA31770.1| ORF 2 (68 AA) (2187 is 2nd base in codon) [Staphylococcus aureus]
>gi|46588|emb|CAA31769.1| beta-hemolysin (AA 1 - 330) [Staphylococcus aureus]
>gi|46587|emb|CAA31768.1| ORF 1 (AA 1 - 121) (1 is 2nd base in codon) [Staphylococcus aureus]
>gi|46582|emb|CAA35680.1| ORF 419 protein [Staphylococcus aureus]
>gi|46581|emb|CAA35679.1| FemA protein [Staphylococcus aureus]
>gi|46580|emb|CAA35678.1| trpA protein (AA at 1) [Staphylococcus aureus]
>gi|46576|emb|CAA26883.1| Methylase (AA 1-11) (172 is 2nd base in codon) [Staphylococcus aureus]
>gi|809753|emb|CAA26103.1| pot. reading frame C (aa 51-230) (1 is 3rd base in codon) [Staphylococcus aureus]
>gi|736294|emb|CAA68826.1| transposase [Staphylococcus aureus]
>gi|671632|emb|CAA78911.1| unknown [Staphylococcus aureus]
>gi|581558|emb|CAA53189.1| isoleucyl tRNA synthetase [Staphylococcus aureus]
>gi|438228|emb|CAA53191.1| ORF C [Staphylococcus aureus]
>gi|438227|emb|CAA53190.1| ORF B [Staphylococcus aureus]
>gi|49313|emb|CAA78910.1| dihydrofolate reductase [Staphylococcus aureus]
>gi|49018|emb|CAA44472.1| ethidium bromide resistance protein [Staphylococcus aureus]
>gi|49017|emb|CAA44471.1| ethidium bromide resistance protein [Staphylococcus aureus]
>gi|46573|emb|CAA38227.1| ermC [Staphylococcus aureus]
>gi|46571|emb|CAA35972.1| staphylococcal enterotoxin C3 [Staphylococcus aureus]

>gi|46567|emb|CAA29260.1| enterotoxin C1 precursor (AA -27 to 239) [Staphylococcus aureus]
>gi|46561|emb|CAA33598.1| ethidium bromide resistance protein (AA 1-107) [Staphylococcus aureus]
>gi|46554|emb|CAA68825.1| ORF 140 [Staphylococcus aureus]
>gi|46553|emb|CAA68824.1| dihydrofolate reductase type S1 [Staphylococcus aureus]
>gi|46552|emb|CAA68823.1| thymidylate synthase [Staphylococcus aureus]
>gi|46550|emb|CAA26107.1| pot. reading-frame C (aa 1-90) (4555 is 2nd base in codon) [Staphylococcus aureus]
>gi|46549|emb|CAA26106.1| pot. reading-frame A (aa 1-315) [Staphylococcus aureus]
>gi|46548|emb|CAA26105.1| reading frame D (aa 1-215) chloramphenicol resistance (CAT) [Staphylococcus aureus]
>gi|46547|emb|CAA26104.1| pot. reading-frame B (aa 1-311) pot. replication protein [Staphylococcus aureus]
>gi|4379429|emb|CAA24584.1| reading frame C (replication) [Staphylococcus aureus]
>gi|1333816|emb|CAA24587.1| reading frame D [Staphylococcus aureus]
>gi|1333815|emb|CAA24585.1| reading frame A [Staphylococcus aureus]
>gi|1333813|emb|CAA34365.1| binR product (no atg) [Staphylococcus aureus]
>gi|806585|emb|CAA89212.1| superoxide dismutase [Staphylococcus aureus]
>gi|581555|emb|CAA26630.1| unidentified reading frame put. function in cat regulation [Staphylococcus aureus]
>gi|398182|emb|CAA34366.1| bin3 product [Staphylococcus aureus]
>gi|397526|emb|CAA79304.1| clumping factor [Staphylococcus aureus]
>gi|46540|emb|CAA35664.1| coagulase precursor [Staphylococcus aureus]
>gi|46537|emb|CAA26631.1| chloramphenicol acetyltransferase [Staphylococcus aureus]
>gi|46534|emb|CAA24586.1| CAT (chloramphenicol resistance) [Staphylococcus aureus]
>gi|809610|emb|CAA01358.1| sau3AI M [Staphylococcus aureus]
>gi|580669|emb|CAA01357.1| sau3AI R [Staphylococcus aureus]
>gi|512508|emb|CAA01068.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512504|emb|CAA01067.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512502|emb|CAA01066.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512500|emb|CAA01065.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512498|emb|CAA01064.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512496|emb|CAA01063.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512493|emb|CAA01062.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512491|emb|CAA01061.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512489|emb|CAA01060.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512487|emb|CAA01059.1| fibronectin binding protein [Staphylococcus aureus]
>gi|412259|emb|CAA00843.1| Arp 4 [Staphylococcus aureus]
>gi|412214|emb|CAA00364.1| structural A protein [Staphylococcus aureus]
>gi|412211|emb|CAA00363.1| structural A protein [Staphylococcus aureus]
>gi|765073|gb|AAA99982.1| autolysin
>gi|765072|gb|AAA99981.1| ORF3
>gi|765071|gb|AAA99980.1| ORF2
>gi|765070|gb|AAA99979.1| ORF1
>gi|790573|gb|AAA99709.1| pyrrolidone carboxyl peptidase
>gi|46602|emb|CAA37814.1| putative transposase (AA 1 - 224) [Staphylococcus aureus]
>gi|153077|gb|AAA98349.1| vgh gene product
>gi|581278|emb|CAA26967.1| ORF [Staphylococcus aureus]
>gi|581277|emb|CAA26960.1| tnpA protein [Staphylococcus aureus]
>gi|43733|emb|CAA26966.1| peptide 1 [Staphylococcus aureus]
>gi|43732|emb|CAA26965.1| peptide L [Staphylococcus aureus]
>gi|43731|emb|CAA26964.1| S-adenosyl-methionine dependent methylase [Staphylococcus aureus]
>gi|43730|emb|CAA26963.1| adenylyltransferase AAD9 (spc) [Staphylococcus aureus]
>gi|43729|emb|CAA26962.1| pot. tnpC protein [Staphylococcus aureus]
>gi|43728|emb|CAA26961.1| pot. tnpB protein [Staphylococcus aureus]
>gi|1255262|gb|AAA96060.1| phosphoenolpyruvate carboxykinase
>gi|1255260|gb|AAA96059.1| o-succinylbenzoic acid (OSB) synthetase
>gi|1255259|gb|AAA96058.1| o-succinylbenzoic acid (OSB) CoA ligase
>gi|46698|emb|CAA26428.1| put. AAD(9) determinant (aa 1-260) [Staphylococcus aureus]
>gi|46697|emb|CAA26427.1| 3' end of tnpC [Staphylococcus aureus]
>gi|46591|emb|CAA43885.1| Sphingomyelinase [Staphylococcus aureus]
>gi|1196899|gb|AAA88547.1| unknown protein
>gi|153000|gb|AAA88550.1| enterotoxin B
>gi|152949|gb|AAA88549.1| transposase
>gi|152948|gb|AAA88548.1| aminoglycoside resistance protein
>gi|152947|gb|AAA88546.1| transposase
>gi|1181627|gb|AAA86871.1| VAT B
>gi|1016770|gb|AAA86131.1| prolipoprotein diacylglycerol transferase
>gi|705406|gb|AAA82984.1| hyaluronate lyase
>gi|1020317|gb|AAA79506.1| S-adenosylmethionine synthetase
>gi|458420|gb|AAA79365.1| proline permease homolog
>gi|1015409|gb|AAA79055.1| Pre protein

>gi|1015408|gb|AAA79054.1| chloramphenicol acetyltransferase
 >gi|1015407|gb|AAA79053.1| cat leader peptide
 >gi|1015406|gb|AAA79052.1| replication initiation protein
 >gi|915308|gb|AAA74889.1| fibrinogen binding protein
 >gi|409241|gb|AAA74375.1| penicillin-binding protein 2
 >gi|153086|gb|AAA73952.1| DNA gyrase A subunit
 >gi|153085|gb|AAA73951.1| DNA gyrase B subunit
 >gi|153084|gb|AAA73950.1| homologue; putative
 >gi|153062|gb|AAA72091.1| helicase
 >gi|153061|gb|AAA72090.1| [pcrA] gene products
 >gi|152957|gb|AAA71898.1| 5-enolpyruvylshikimate-3-phosphate synthase
 >gi|152956|gb|AAA71897.1| 3-phosphoshikimate-1-carboxyvinyltransferase
 >gi|152955|gb|AAA71896.1| 3-dehydroquinate synthase
 >gi|845687|gb|AAA67855.1| lacA repressor, putative
 >gi|845686|gb|AAA67853.1| ORF-27
 >gi|153035|gb|AAA67854.1| lacR repressor
 >gi|567036|gb|AAA64644.1| CapE
 >gi|506709|gb|AAA64652.1| CapM
 >gi|506708|gb|AAA64651.1| CapL
 >gi|506707|gb|AAA64650.1| CapK
 >gi|506706|gb|AAA64649.1| CapJ
 >gi|506705|gb|AAA64648.1| CapI
 >gi|506704|gb|AAA64647.1| CapH
 >gi|506703|gb|AAA64646.1| CapG
 >gi|506702|gb|AAA64645.1| CapF
 >gi|506700|gb|AAA64643.1| CapD
 >gi|506699|gb|AAA64642.1| CapC
 >gi|506698|gb|AAA64641.1| CapB
 >gi|506697|gb|AAA64640.1| CapA
 >gi|684950|gb|AAA62477.1| staphylococcal accessory regulator A
 >gi|567884|gb|AAA53114.1| lysyl-tRNA synthetase
 >gi|561880|gb|AAA53116.1| gyrase-like protein alpha subunit
 >gi|561879|gb|AAA53115.1| gyrase-like protein beta subunit
 >gi|463285|gb|AAA50463.1| putative
 >gi|551992|gb|AAA26680.1| 25 kD protein (putative); putative
 >gi|551991|gb|AAA26674.1| enterotoxin B
 >gi|495089|gb|AAA26675.1| recombinase
 >gi|398085|gb|AAA26683.1| acetyltransferase
 >gi|153125|gb|AAA26684.1| ATP-binding protein
 >gi|153123|gb|AAA26682.1| toxic shock syndrome toxin-1 precursor
 >gi|153121|gb|AAA26681.1| staphylococcal enterotoxin A precursor
 >gi|153115|gb|AAA26678.1| tetM
 >gi|153106|gb|AAA26677.1| protein A (ttg start codon)
 >gi|153104|gb|AAA26676.1| protein A (ttg start codon)
 >gi|153100|gb|AAA26673.1| Sau3AIM protein
 >gi|153099|gb|AAA26672.1| Sau3AIR protein (ttg start codon)
 >gi|153097|gb|AAA26671.1| bleomycin resistance protein
 >gi|153096|gb|AAA26670.1| neomycin resistance protein
 >gi|153090|gb|AAA26669.1| REP N protein (rep N)
 >gi|153088|gb|AAA26668.1| ethidium resistance protein (ebr)
 >gi|153082|gb|AAA26667.1| recombination and repair protein
 >gi|153080|gb|AAA26666.1| resistance protein
 >gi|153079|gb|AAA26665.1| transposase
 >gi|153067|gb|AAA26662.1| peptidoglycan hydrolase
 >gi|153057|gb|AAA26659.1| nuclease precursor
 >gi|153055|gb|AAA26658.1| norA
 >gi|537341|gb|AAA26647.1| beta-lactamase
 >gi|537340|gb|AAA26646.1| beta-lactamase
 >gi|537339|gb|AAA26645.1| beta-lactamase
 >gi|537338|gb|AAA26644.1| beta-lactamase
 >gi|537337|gb|AAA26643.1| beta-lactamase
 >gi|537336|gb|AAA26642.1| beta-lactamase
 >gi|475839|gb|AAA26654.1| leucocidin S component
 >gi|393266|gb|AAA26634.1| glycerol ester hydrolase
 >gi|295156|gb|AAA26639.1| gamma-hemolysin component B
 >gi|295155|gb|AAA26638.1| gamma-hemolysin component C
 >gi|295154|gb|AAA26637.1| gamma-hemolysin component A
 >gi|295152|gb|AAA26632.1| fibronectin-binding protein precursor
 >gi|153045|gb|AAA26653.1| prolipoprotein signal peptidase
 >gi|153041|gb|AAA26651.1| lincosaminide nucleotidyltransferase
 >gi|153039|gb|AAA26650.1| phospho-beta-galactosidase (lacG)

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>gi|153038|gb|AAA26649.1|enzyme II-lac (lacE)
>gi|153037|gb|AAA26648.1|enzyme III-lac (lacF)
>gi|153033|gb|AAA26641.1|tagatose 6-phosphate isomerase
>gi|153027|gb|AAA26640.1|DNA invertase (ttg start codon)
>gi|153025|gb|AAA26636.1|gyrase A
>gi|153024|gb|AAA26635.1|gyrase B
>gi|153020|gb|AAA26633.1|lipase precursor (geh; EC 3.1.1.3)
>gi|295151|gb|AAA26623.1|enterotoxin
>gi|295149|gb|AAA26622.1|enterotoxin
>gi|295147|gb|AAA26621.1|enterotoxin
>gi|295145|gb|AAA26620.1|enterotoxin
>gi|295143|gb|AAA26619.1|enterotoxin
>gi|295141|gb|AAA26618.1|enterotoxin
>gi|153012|gb|AAA26628.1|ETB precursor
>gi|153008|gb|AAA26626.1|epidermolytic toxin A precursor
>gi|153006|gb|AAA26625.1|ETA precursor
>gi|153004|gb|AAA26624.1|enterotoxin C3
>gi|153002|gb|AAA26617.1|enterotoxin type E precursor
>gi|152998|gb|AAA26616.1|epidermal cell differentiation inhibitor
>gi|152982|gb|AAA26613.1|chloramphenicol acetyltransferase
>gi|152981|gb|AAA26612.1|precursor protein
>gi|152979|gb|AAA26611.1|putative
>gi|152978|gb|AAA26610.1|E1-E2 cadmium efflux adenosine triphosphatase
>gi|152977|gb|AAA26609.1|cadmium resistance protein
>gi|152976|gb|AAA26608.1|125 codon reading frame that is similar to Tn554-encoded TnpC; RBS
retained, but no evidence as to whether transcribed or expressed; putative
>gi|152975|gb|AAA26607.1|630 codon reading frame resembling tnpB of Tn554; transcription or
translation signals upstream of the reading frame removed by the deletion noted above; presumed to
be vestigial and not expressed; putative
>gi|152974|gb|AAA26606.1|29 codon reading frame of which N-terminal 25 are similar to the
corresponding region of Tn554-encoded TnpA; TnpA is truncated by a 1006 bp deletion and is presumed
inactive; putative
>gi|152970|gb|AAA26605.1|beta-lactamase repressor
>gi|152953|gb|AAA26598.1|alpha-hemolysin
>gi|152951|gb|AAA26597.1|accessory gene regulator protein
>gi|152945|gb|AAA26596.1|aminocyclitol-3'-phosphotransferase
>gi|152967|gb|AAA21184.1|ORF
>gi|295159|gb|AAA21183.1|putative
>gi|295158|gb|AAA21182.1|mecR
>gi|387880|gb|AAA20874.1|collagen adhesin
>gi|310604|gb|AAA18516.1|ORF3
>gi|310603|gb|AAA18515.1|ORF2
>gi|310602|gb|AAA18514.1|ORF1
>gi|409063|gb|AAA17490.1|exfoliative toxin A
>gi|152985|gb|AAA16529.1|chloramphenicol acetyltransferase
>gi|152984|gb|AAA16528.1|precursor protein
>gi|458428|gb|AAA16512.1|FtsZ
>gi|425478|gb|AAA16442.1|phosphatidylinositol-specific phospholipase C
>gi|153053|gb|AAA16158.1|norA1199 protein
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TABLE 7 : MAP AND SEQUENCE POSITION OF THE 73 ORFs PREDICTED TO BE ENCODED BY PHAGE 44AHJD THAT ARE GREATER THAN 33 AMINO ACIDS

Phage 44AHJD ORFs list

nb	Name	Frame	Position	Size (a.a.)	Key words
1	44AHJDORF001	-1	10342..12627	761	DNA polymerase;
2	44AHJDORF002	3	3789..5732	647	Techoic acid; Staph;
3	44AHJDORF003	2	6626..8389	587	Tail;
4	44AHJDORF004	1	8764..10227	487	Serine protease motif;
5	44AHJDORF005	-1	12643..13890	415	
6	44AHJDORF006	2	803..2029	408	
7	44AHJDORF007	1	2044..3027	327	Upper collar;
8	44AHJDORF008	2	3020..3775	251	Lower collar;
9	44AHJDORF009	2	5744..6496	250	Amidase; Staph;
10	44AHJDORF010	-2	13938..14420	160	
11	44AHJDORF012	3	8391..8813	140	Holin;
12	44AHJDORF013	-2	14586..14996	136	
13	44AHJDORF113	1	199..600	133	
14	44AHJDORF011	-2	15225..15593	122	
15	44AHJDORF114	-2	15870..16172	100	
16	44AHJDORF014	3	6243..6521	92	
17	44AHJDORF015	1	15403..15645	80	
18	44AHJDORF016	-1	15616..15852	78	
19	44AHJDORF017	-2	10536..10757	73	
20	44AHJDORF018	-1	886..1098	70	
21	44AHJDORF019	-2	9630..9836	68	
22	44AHJDORF121	-1	16165..16362	65	
23	44AHJDORF020	2	13865..14053	62	
24	44AHJDORF123	2	614..796	60	
25	44AHJDORF021	-2	5634..5816	60	
26	44AHJDORF023	-2	6315..6494	59	
27	44AHJDORF024	1	14275..14451	58	
28	44AHJDORF025	-3	14999..15175	58	
29	44AHJDORF026	-3	14426..14593	55	
30	44AHJDORF027	1	12916..13080	54	
31	44AHJDORF029	-1	15019..15183	54	
32	44AHJDORF028	-3	9071..9235	54	
33	44AHJDORF030	3	14487..14648	53	
34	44AHJDORF031	2	11039..11191	50	
35	44AHJDORF135	3	693..842	49	
36	44AHJDORF033	-1	3646..3795	49	
37	44AHJDORF032	-2	9306..9455	49	
38	44AHJDORF034	-3	14000..14146	48	
39	44AHJDORF035	-3	13811..13957	48	
40	44AHJDORF036	-3	10019..10165	48	
41	44AHJDORF022	-3	8468..8611	47	
42	44AHJDORF037	1	14788..14931	47	
43	44AHJDORF038	-2	3528..3671	47	
44	44AHJDORF039	3	1743..1883	46	
45	44AHJDORF040	2	9740..9877	45	
46	44AHJDORF041	2	15836..15973	45	
47	44AHJDORF042	-1	5014..5151	45	
48	44AHJDORF043	-1	4402..4539	45	
49	44AHJDORF044	-2	12783..12917	44	
50	44AHJDORF149	-2	639..770	43	
51	44AHJDORF046	1	4891..5019	42	
52	44AHJDORF047	1	11911..12039	42	
53	44AHJDORF045	2	10655..10783	42	
54	44AHJDORF048	-3	15212..15340	42	
55	44AHJDORF049	3	5784..5909	41	
56	44AHJDORF050	3	13158..13283	41	
57	44AHJDORF051	-2	10944..11066	40	
58	44AHJDORF052	-3	14216..14338	40	

TABLE 8: NUCLEOTIDE AND PREDICTED AMINO ACID SEQUENCE OF ALL 73 ORFs IDENTIFIED IN PHAGE 44 AHJD

44AHJDORF001

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12627 atgggattactagaatgcatgcaatatcataaacatgaacgtcgaatgattttatactgggatatagaacattagcgtacaat
1 M G L L E C M Q Y H K H E R R M I L Y W D I E T L A Y N
12543 aaagttaacggacgaaaaaaaccaacaaatataaaaacgttacttattctgtagcaattgggttggttaaatgggttatgaaatt
29 K V N G R K K P T K Y K N V T Y S V A I G W F N G Y E I
12459 gatgttgaagtattttccgagtttcgaatctttttatgacgcattttatcgtatgtgaaaagacgtgatacaatcacaaaatca
57 D V E V F P S F E S F Y D A F Y T Y V K R R D T I T K S
12375 aaaacagatattatcatgattgcacataactgtaataaatacgataatcattttttacttaagacaccatgcgttattttgat
85 K T D I I M I A H N C N K A Y D N H F L L K D T M R Y F D
12291 aatattacacgcgaaaaatataatattttaaactctgcagaagaaaatgaacacacattaaaaatgaagaggctactatttttagcc
113 N I T R E N I Y L K S A E E N E H T L K M K E A T I L A
12207 aaaaatcaaaatgtaattttagaaaaacgtgttaaatcttcaatcaatttagatttaacaatgttttttaaatgggttttaaat
141 K N Q N V I L E K R V K S S I N L D L T M F L N G F K F
12123 aatattatgataactttatgaaaaccaatcatcaattgcaacattaggtgaagaattacttgatgggtggttatttaacagaa
169 N I I D N F M K T N T S I A T L G K K L L D G G Y L A
12039 tcacaacttaaaacagatttttaattatcagatttttgataaagataatgatgatagtgaaagcctatgactatgctgtg
197 S Q L K T D F N Y T I F D K D N D M N D S E A Y D Y A V
11955 aaatgttttgcaaaactcacactgaacaacttacatcattcataatgacgtgattatattaggtatgtgccattatcattat
225 K C F A K L T P E Q L T Y I H N D V I I L G M C H I H Y
11871 agtgatatatttccaaattttgactatacaaaattaacattttcattgaatattatggaatcttactgaaataatgaaatgaca
253 S D I F P N F D Y N K L T F S L N I M E S Y L N N E M T
11787 cgttttcagttactcaaccaatcatcaagatattttaaatactttatcacattatcatttccatgatatgaatttttatgactat
281 R F Q L L N Q Y Q D I K I S Y T H Y H F H D M N F Y D Y
11703 attaaatcattctatcgtgggtggttttaaatatgtataacaccaaatacataaaactaattgatgagccttgtttttctatt
309 I K S F Y R G G L N M Y N T K Y I N K L I D E P C F S I
11619 gacatcaatcgagttatccttattgtgatgtatcagaaaaattccaacatgggtataacttttacgaacactattcagaacca
337 D I N S S Y P Y V M Y F Y H E K I P T W L Y F Y E H Y S E P
11535 acgttaatccctacttttttagatgatgacaattatttttcattatataagattgataaagatgtatttaacgatttaattatta
365 T L I P T F L D D D N Y F S L Y K I D K D V F N D D L L
11451 attaaaattaaatcacgtgtattacgtcaaatgattgtaaaatactataataatgataatgattacgttaatatcaatacaaat
393 I K I K S R V L R Q M I F Y N Y N N D Y V N I N T N
11367 acattaagaatgattcaagacattacgggtattgattgcacatatacgtgttaattcgtttgttatatatgaattgtaatac
421 T L R M I Q D I T G I D C M H I R V N S F V I Y E C E Y
11283 tttcatgcacgtgatattatttttcaaaactattttattaaaacacaaaggttaagttaaaaacaaaatcaatatgacatcacct
449 F H A R D I I F P Q N Y F I K I P T G K L K N K I N M T S P
11199 taogactatcacattactgatgatatacaacgaacacccatactcaaatgaggagggttatgttatctaaagtcgttttaaatgga
477 Y D Y H I T D D I N E H P Y S N E E V M L S K V V L N G
11115 ttatatggcatacctgcattacgttcacatttttaacttattccgttttagatgataacaatgaactatacaatatcattaacgggt
505 L Y G I P A R S H F N L F R L D D N N E L Y N I I N G
11031 taaaaaaacactgaacgtaatatattttctctacatttgcacatcacgttcattgtataacttattgggttcccttccaatac
533 Y K N T E R N I L F S T F V T S R S L Y N L L V P F Q Y
10947 ttaacggaaagtgaattgacgacaattttattttatgcgatactgatagtttggatatgaaatccgttggttaaaccttattg
561 L T E S E I D D N F I Y C D T D S L Y M K S V V K P L L
10863 aaccccgattttatcgaccgatagccttaggttaaatgggatattgaaaacgaacagatagataagatgtttgtgactgaatcat
589 N P S L F D P I A L G K W D I E N E Q I D K M F V L N H
10779 aagaaatgcatatgaagtgaatggaaagattaaaattgcttctgctggtataccgaaaaacgcctttgatacaagcgtcgat
617 K K Y A Y E V N G K I A S A G I P K N A F D T S V D
10695 tttagaacctttgtacgtgaacaattctttgacggtgccattattgaaaacataaaaagtatctataatgagcaactgaataa
645 F E T F V R E Q F F D G A I I E N N K S I Y N E Q G T I
10611 tcgatataatccgtctaaaactgaaattgtatgtggaatgtatgatgaatattttactgatgaacttaatatgaaacgtgaa
673 S I Y P S K T E I V C G N V Y D E Y F T D E L N M K R E
10527 tttatattaaaagacgctagagaaaaatttcgaccatagtcaatttgatgatattctttatattgaaagtgacatcggttcattt
701 F I L K D A R E N F D H S Q F D D I L Y I E S D I G S F
10443 tcacttaacgacttatttccagttgaacgttcagtacataacaaatctgatttgcataatataaaacgtgaacatgatgaata
729 S L N D L F P V E R S V H N K S D G L H I L K R E H D E I
10359 aaaaaaggcaactgttaa 10342
757 K K G N C *

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44AHJDORF002

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3789 atggcatataatgaaaacgatttttaaatattttgatgacattcgtccatttttagacgaaattttataaaacgagagaacgttat
1 M A Y N E N D F K Y F D D I R P F L D E I Y K T R E R Y
3873 acaccgttttacgatgatagacgagattataataactaattcaaaatcatattatgattatatttcaagattatcaaaactaatt
29 T P F Y D D R A D Y N S K S Y Y D Y I S R L S K L I
3957 gaagtattagcacgtcgtattttgggactatgacaatgaattaaaaaacgtttcaaaaattgggacgacttaatgaagcattt
57 E V L A R R I W D Y D N E L K K R F K N W D D L M K A F
4041 ccagagcaagcgaaagacttatttagagggttggttaaacgacggtacgattgacagtattattcatgacgagtttaaaaaatat
85 P E Q A K D L F R G W L N D G T I D S I I H D E F K K Y
4125 agcgcaggattaacatcgccatttgcgttttaaaagtactgaaatgaaacaaatgaatgactttaatcagaagttaaagac

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113 S A G L T S A F A L F K V T E M K Q M N D F K S E V K D
 4209 ttaattaaagatattgacggtttcgtaaatgggtttgaattaaatgagcttgaaccaaagtttgatgggctttgggtgatt
 141 L I K D I D R F V N G F E L N E L E P K F V M G F G G I

 4293 cgcaacgcagttaaccaatctattaattgataaagaacaaatcacatgtactctacacaatccgattctcaaaaacctgaa
 169 R N A V N Q S I N I D K E T N H M Y S T Q S D S Q K P E
 4377 ggtttttggataaataaattaacacctagtggtgacttaatttcaagcatgcgtattgtacagggtggtcatggtacaacaatc
 197 G F W I N K L T P S G D L I S S M R I V Q G G H G T T I
 4461 ggattagaacgtcaatccaatggtgaaatgaaaatctggttacatcacgatggtggtgcaaaactgttacaagtcgcatataaa
 225 G L E R Q S N G E M K I W L H H D G V A K L L Q V A Y K
 4545 gataattatgtatttagatttagaagaggctaaagggttaacagattatacaccacagtcacttttaacaaacacacatttaca
 253 D N Y V L D L E E A K G L T D Y T P Q S L L N K H T F T
 4629 ccgtaattgatgaagcaaatgacaaactcattttaagattcggtgacggaacaatacagggttcgttcaagagcagacgtaaaa
 281 P L I D E A N D K L I L R F G D G T I Q V R S R A D V K
 4713 aatcacattgatgaatgtagaaaaagaatgacaattgataattcagaaaaaatgataatcgttggatgcaaggcattgtcgtt
 309 N H I D N V E K E M T I D N S E N N D N R W M Q G I A V
 4797 gatggtgatgatttatactggttaagtggttaacagttcagttacatggttcaaatcggttaaatattcattaaacacaggt
 337 D G D D L Y W L S G N S S V N S H V Q I G K Y S L T T G
 4881 caaaagatttatgattatccatttaagttatcatatcaagacggtattaatttcccacgtgataacttttaagagcctgagggt
 365 Q K I Y D Y P F K L S Y Q D G I N F P R D N F K E P E G
 4965 atttgatttatacaaatccaaaaacaaacgtaaatcggttacttgctatgacaaacggcggtggtgaaaaacggttccat
 393 I C I Y T N P K T K R K S L L L A M T N G G G G K R F H
 5049 aatttatatggtttcttccaacttggtgagatgaacactttgaagcattacgcgcaagaggttcacaaaactataaattaaca
 421 N L Y G F Q L G F E H F E A L R A R G S Q N Y K L V
 5133 aaagacgacggtcggtgacttatctattccagaccattcgacatttaaatgacttaacgcaagctggtttttatttatattgac
 449 K D D G R A L S I P D H I D D L N D L T Q A G F Y Y I D
 5217 gggggtactgcagaaaaacttaagaatatgccaatgaatggttagcaagcgtataattgacgctggttgtttcattaatgtatac
 477 G G I A E K N M P M N G S K R I I D A G C F I N Y
 5301 cctacaacacaaacttaggtacggttcaagaattaacacggtttctcaacaggtcgtaaaatggttaaaatggtgcgtggtatg
 505 P T T Q T L G T V Q E L T R F S T G R K M V K M V R G M
 5385 acttttagacgtatttacgttaaaatgggattatggattatggacaacaatcaaaactgacgcaccatcatcaagaatatttgaa
 533 T L D V F T L K W D Y G L W T T I K T D A P Y Q E Y L E
 5469 gcaagtcaatacaataactggattgcttatgtaacaacagctggtgagttacattacaggttaaccaaattggaattatttaga
 561 A S Q Y N N W I A Y V T T A G E Y Y I T G N Q M E L F R
 5553 gacgcgcgaagaataaaaaagtggtgcatggttacgtgtgtcaagtgttaacgcagtcggtgaagtaagacaaacatta
 589 D A P E E I K K V G A W L R V S S G N A V G E V R Q T L
 5637 gaggtcaatatatcggaatataaagaattcttcagtaattgtaatgcggaacaaaacatcgtaatatggttgggtagcaaaa
 617 E A N I S E Y K E F F S N V N A E T K H R E Y G W V A K
 5721 catcaaaaatag 5732
 645 H Q K *

44AHJDORF003

6626 atgagaaagtttaacgaatttttaagtttttctataacacaccggtttacagactatcaaaacacgattcatttttaatagtaataaa
 1 M R K L T N F K F F Y N T P F T D Y Q N T I H F N S N K
 6710 gaacgtgatgattattttttaaatggtcggtcatttttaaatcggttagactattcaaaacaacggtataattttatagctgataga
 29 E R D D Y F L N G R H F K S L D Y S K Q P Y N F I R D R
 6794 atggaatcaatggtgatagcagtggtgacgcacaaaggttaactacatgacgtttttatcagattttgaggtatagaaga
 57 M E I N V D M Q K H D Y G L V S G I N Y M T F L S D F E D R R
 6878 tattacgcttttgaaccaaatacgaatcggtgaatgacgttggtttaaataatattttgtcattgataccattatgacgtat
 85 Y Y A F F V N Q I E Y V N D V V V K I Y F V I D T I M T Y
 6962 acacaagggaatgtattagagcaactctcaaacgtcaatattgaacgtcaacattttcaaaacgcacgtataactatatgtta
 113 T Q G N V L E Q L S N V N I E R Q H L S K R T Y N Y L
 7046 ccaatgttacgtaataatgatgatgtgttaaaagtatcaataaaaaactatgtttataaccaaatacacaataatttggaataat
 141 P M L R N N D D V L K V S N K N Y V Y N Q M Q Q Y L E N
 7130 ttagtattattccagtcagcgtgatttatcaagaaatttggtactaaaaagagccaaacttagatacgtcaaaagggtacg
 169 L V L F Q S S A D L S K K F G T K K E P N L D T S K G T
 7214 atttatgacaatatcacatcaccagtcacacttatacgttatggaatattggtgactttattaaactttatggataaaatgagtgcc
 197 I Y D N I T S P V N L Y V M E Y G D F I N F M D K M S A
 7298 tatccatggattacgcaaaactttcaaaagggttcaaatgttacctaaagactttattaatacaaaagacttagaggacgttaaa
 225 Y P W I T Q N F Q K V Q M L P K D F I N T K D L E D V K
 7382 accagtgaaaaaattacaggattaaaaacattaaaaacagggtggttaaatcaaaagaatggagtctaaaagatttatcattaagt
 253 T S E K I T G L K T L K Q G G K S K E W S L K D L S L S
 7466 ttctcaaatcttcaagagatgatgttatcaaaaaagatgaatttaaacatatgatacgttaagtagtatgacaattgtaatt
 281 F S N M L Q E M M L S K K D E F K H M I R N E Y M T I E F
 7550 tatgactggaatggaataacgatgttactcgacgctggttaagatttcacaaaaaactggtgttaagttacgtacaaaatcaatt
 309 Y D W N G N T M L L D A G K I S Q K T G V K L R T K S I
 7634 attggttatcataatgaagttcgagtatatccagtagattataacagtgctgaaaacgacagaccaataactcgctaaaaataaa
 337 I G Y H N E V R V Y P V D Y N S A E N D R P I L A K N K
 7718 gaaatattgattgatacgggttcattcttaatacaaatataacatttaattagttttgcacaagtaccaatattaatcaataat
 365 E I L I D T G S F L N T N I T F N S F A Q V P I L I N N
 7802 ggtatcttaggacaatcacaacaagccaacggacaaaaaagtcagaaagtcatttaattacaaatcgatttgataatgtatta
 393 G I L G Q S Q Q A N R Q K N A E S Q L I T N R I D N V L

44AHJDORF008

3020 atggctagatcacacaatgactttatagcatttcattaaatcagaattgattaaaaaagggtttcaatgaatttgtaaatgataat
1 M A R Y T M T L Y D F I K S E L I K K G F N E F V N D N
3104 aaattaacggtttatgatgatgaatttcaattcatgcaaaaaatgctgaagttcgacaaagacgttttagctatcgttaaatgaa
29 K L T F Y D D E F Q F M Q K M L K F D K D V L A I V N E
3188 aaagtatttaaagggttttcattgaaagatgaattatcagatttacttttaaaaaatcatttacgattcatttttttagataga
57 K V F K G F S L K D E L S D L L F K K S F T I H F L D R
3272 gaaatcaacagacaacagttgaagcatttggcatgcaagtgattactgtatgtattacacatgaggattatttaaatgtgggt
85 E I N R Q T V E A F G M Q V I T V C I T H E D Y L N V V
3356 tattcatcaagtgaagttgaaaaatacttacatcacaaaggcttcacagaacacaatgaagatacaacaagtaacactgatgaa
113 Y S S S E V E K Y L Q S Q G F T E H N E D T T S N T D E
3440 acatcgaatcaaaatgctacatcttttagacaattcaactggcatgactgcaaacagaaacgcttatgtgtcattaccacaaagt
141 T S N Q N A T S L D N S T G M T A N R N A Y V S L P Q S
3524 gaggttaacattgatgttgataatacaacggttacgattcgctgataataatcagattgataacggttaaaactgtgaataaatcg
169 E V N I D V D N T T L R F A D N N T I D N G K T V N K S
3608 agtaacgaaagtaatacaaacgcaaaacgtaatacaaaatggaaggttaacacaaaggtacacaaatcactaagcagatttta
197 S N E S N Q N A K R N Q N Q K G N A K G T Q F T K Q Y L
3692 attgataatattgataaagcgtacgatttaagaaagaaaatttttaaatgaatttgataaaaaatgtttttacaaatttgtag 3775
225 I D N I D K A Y D L R K K I L N E F D K K C F L Q I W *

44AHJDORF009

5744 atgaaatcacacaacaagcaaaagaatggatatataagcatgagggggcaggtgtgactttgatggtgcatatggatttcaa
1 M K S Q Q Q A K E W I Y K H E G A G V D F D G A Y G F Q
5828 tgtatggacttatcagttgcttattacattactgacggttaaagttcgcatgtgggttaagctaaagacgcgataaat
29 C M D L S V A Y V Y Y I T D G K V R M W G N A K D A I N
5912 aatgacttttaaagggttttagcgacggtgtataaaaaatcacccgagctttaaacctcaattaggggacgttgctgtatatacaaat
57 N D F K G L A T V Y K N T P S F K P Q L G D V A V Y T N
5996 ggacaaagcattagaaacatcaaaagtaaatcattggaaggttaattattattacatgcttagaacaacaaactggttaggcggcggt
85 G Q Y G H I Q C V L S G N L D Y Y T C L E Q N W L G G G
6080 tttgacggttgggaaaaagcaaccatttagaacacattattatgacggtgtaactcactttattagacctaaattttcaggtagt
113 F D G W E K A T I R T H Y Y D G V T H F I R P K F S G S
6164 aatgcaaaagcattagaaacatcaaaagtaaatcattggaaggttaattattattacatgcttagaacaacaaactggttaggcggcggt
141 N S K A L E T S K V N T F G K W K R N Q Y G T Y Y R N E
6248 aatgggtacatttatcatgtgtgtttttacaaatatttgcacgtgtcggttagtcctaaattatcagaacctaatggctattgtgttc
169 N G T F T C G G F L P I F A R V G S P K L S E P N G Y W F
6332 caaccaaacggttatataacgtaaatggttttattcagatggtttaggttataactgggcaaggcacacgt
197 Q P N G Y T P Y N E V C L S D G Y V W I G Y N W Q T R
6416 tattatttaccagtgcccaatggaatggaaaaacaggttaattagttacagtggttattccttgggggggtgttctcataa 6496
225 Y Y L P V R Q W N G K T G N S Y S V G I P W G V F S *

44AHJDORF010

14420 ttgggttagacatagctctgaaatggatagatggaaaaaagagaagctagaaaagagcaagaaaaagattttattttaaat
1 L V R H T S E M D R W K K E R E A R K E Q E K D L F L N
14336 gatttttagtaattgtaatttttaatttgatgataaagatttacaagaggcgtagattgacacatggaacattttgcacatctg
29 D F S N V N F K F D D K D L Q E A Y I D T W K H F A H L
14252 ccctattttcctaaagaaagaaacgtatcatatgtaaatgctgtatcatttggaagaggttcaagacataaaaaattaaattat
57 P Y F P K E R N V S Y V N A V S L V R G S R H K K L N Y
14168 attcttgaaatataaacgtaaatgatgatttctaatttcaaaacgctaaaaagcataaatacgttttatataatttacaagct
85 I L E I Y N R N D D S N N K N A K K H K Y A L Y N L A
14084 aaaaaataaattcttcaatgtataaataatattaagaaatcgatactttatataaagaaatttggttaaatcagatagaccagtg
113 K N N N S S M Y K Y I K E I D T L Y K E I G K S D R P V
14000 acaaatattgatgataagatgtgaggtataactttttatattatgcaacatttgacgaataa 13938
141 T N I D D E D V R Y N F L Y Y A T F D E *

44AHJDORF011

15593 atgacaacgtaaaagatattttatcaagacacccaaaacacatttagcgagatttgaaatttgaggaaaaaagagaattttatc
1 M T N V K D I L S R H Q N T L A R F E F E E K E R E F I
15509 aaactatcagaattagtagaaaaatacgggtatgaaaaagagtatatcggttagagcattattcacaaacaaagaatcaaaattc
29 K L S E L V E K Y G M K K E Y I V R A L F T N K E S K F
15425 ggtgaacaagggtttatcgctcactgatgactataacgtaaactaacgaaccacttaacagaattaattaaagaaatgagagca
57 G E Q G V I V T D D Y N V N L P N H L T E L I K E M R A
15341 gatgaggacgttgttgacattatcaatgctggagaagttcaattcacattttatgaatatgaaaacaaaaagggtcaaaaagggt
85 D E D V V D I I N A G E V Q F T I Y E Y E N K K G Q K G
15257 tactcaatcaatttttggtcaaggtatcattttaa 15225
113 Y S I N F G Q V S F *

44AHJDORF012

8391 atgaacgaagtaaaattcagattttacagactcagaagcgtttcacatgtttatatacgtgggattttaaaattactctacttt
1 M N E V K F R F T D S E A F H M F I Y A G D L K L L Y F
8475 ttatttgatttaattgttcgttgatattattacaggtattttcaaaagcaattaaaaataataacttatgggtcaaaaaatcaatg
29 L F V L M F V D I I T G I S K A I K N N N L W S K K S M
8559 agaggattttctaaaaaattattgatattctgtattatcatttttagcaaacatcattgaccagattttacaattaaaaagggtggt
SD-138950.1

57 R G F S K K L L I F C I I I L A N I I D Q I L Q L K G G
8643 ctactcatgattacaatattttattatattgcaaatgagggactttctattgtagaaaattgtgcagaaatggacgtattagta
85 L L M I T I F Y Y I A N E G L S I V E N C A E M D V L V
8727 ccagaacaaattaaagataaattaaagagtcattaaaaatgatactgaaaagagtgataacaatgaacgatcaagagaagataga
113 P E Q I K D K L R V I K N D T E K S D N N E R S R E D R
8811 taa 8813
141 *

44AHJDORF013

14996 atgaaaattaaaactacttttagattaataatattaatttattaccttttaacaaatagagattattataatgataaatttgaa
1 M K I K T T F R L N N L I Y Y L L T N R D Y Y N D K F E
14912 aaatttacttcatctaataaaaaatgtatagtaaaaaataaatatgggtgatgtgtatattgagtttgacaaacaatatgatgat
29 K F T S S N K K C I V K I N M G D V Y I E F D K Q Y D D
14828 tttgaaattgaaaaagagttattttagatattcgacattgatattaaaaaacatgtttttaataatacttattttattat
57 F E I E K E L F T L D I D I D I K K H V F N I L V F Y Y
14744 agaaattatttaagtaaatgaattaataagagaaattttattaaacgttacaattgacgacgtattatcaaattttgataaacct
85 R N Y L S N E L I R E I L L N V T I D D V L S N F D K P
14660 cttgaaagcgaattaatgattattttatcaaaacaaagtcataacgataatgggaaagtgattgaccatgaataa 14586
113 L E S E L M I I Y Q N K V I Y D N G K V I D H E *

44AHJDORF113

199 atgacagaatttgatgaaatcgtaaaaccagacgcagacaaagaagaaacttcagaatcaactgaagaaaatttagaatcaactgaa
1 M T E F D E I V K P D D K E E T S E S T E E N L E S T E
283 gaaacttcagaatcaactgaagaatcaactgaagaatcaactgaagaatcaactgaagataaaacagtagaacaacatcgaagaa
29 E T S E S T E E S T E E S T E E S T E D K T V E T I E E
367 gaaaatgaaaacaattagaacctactacaacagatgaagatagttcgaaatttgaccctgttgattagaacaacgtattgct
57 E N E N K L E P T T T D E D S S K F D P V V L E Q R I A
451 tcattagaacaacaagtgactacttttttatcttcacaaatgcaacaaccacaacaagtagacaacaacacaatcagatgtaaca
85 S L E Q Q V T T F L S S Q M Q Q P Q Q V Q Q T Q S D V T
535 gaatcaaaacaaagaagataacgactattcagatgaagaactagttgataagtttagatttagattag 600
113 E S N K E D N D Y S D E E L V D K L D L D *

44AHJDORF114

16172 atgggttaatttgataatgcaccagaaagaaaaggacaaagcctatactgaaatggtgcaactattcaataaactgattcaatgg
1 M V N V D N A P E E K G Q A Y T E M L Q L F N K L I Q W
16088 aatccagcttatacatatttgacaatgcaattaaacttattatcggttgccaacaactattattaaactataatgttctgtt
29 N P A Y T F D N A I N L L S A C Q Q L L L N Y N S S V V
16004 caattcttaaatgatgaactaaacaacgaaactaaaccagaatcaatattgtcttatattgctggtgatgacccaatagaacaa
57 Q F L N D E L N E T K P E S I L S Y I A G D D P I E Q
15920 tggaaatgcataaaggattttatgaaacgtataacgctttacgttttttag 15870
85 W N M H K G F Y E T Y N V Y V F *

44AHJDORF014

6243 atgaaaatggtacatttcatgtggttttttaccatattttgacagtgctggttagtccaaaattatcagaacctaattggctatt
1 M K M V H L H V V F Y Q Y L H V S V V Q N Y Q N L M A I
6327 ggttccaaccaaacggttatacccatataacgaagtttgtttatcagatggttacgtattggttataactggcaaggca
29 G S N Q T V I H I T K F V Y Q M V T Y G L V I T G K A
6411 cacgttattatttaccagtgcccaatggaatggaaaaacaggttaatagttacagtggttattccttggggggtgttctcat
57 H V I I Y Q C A N G M E K Q V I V T V L V F L G G C S H
6495 aatgggtatttttagcctttttctttga 6521
85 N G Y F S L F L *

44AHJDORF015

15403 gtgacgataaacaccttggttcacgaattttgattctttgtttgtgaataatgctctaacgatataactctttttcataccgta
1 V T I T P C S P N F D S L F V N N A L T I Y S F F I P Y
15487 ttttctactaattctgatagtttgataaattctctttttctcctcaaatcaaatctcgctaattgtgttttggtgtcttgat
29 F S T N S D S L I N S L S F S S N S N L A N V F W C L D
15571 aaaatatcttttacgtttgtcattttatttctcctcttatttaaattatttgctttctgcaattgcgatttgtag 15645
57 K I S F T F V I L N F L L F K L F A F C N C D L *

44AHJDORF016

15852 atgaaagttgacgacattgttaccttacgtgtcaaaggttatatacttcattacttagatgatgataatgaatacattgaggaa
1 M K V D D I V T L R V K G Y I L H Y L D D D N E Y I E E
15768 tttttaccacttcacgagtatctttaaccaaaacaaagcaaaagaaattattaccagacacatgtaaacattgtccactaca
29 F L P L H E Y H L T K T Q A K E L L P D T C K L L S T T
15684 cgcacaacgaaaacaattcaagtttattacaatgatttactacaaatcgcaattgcagaaagcaataa 15616
57 R T T K T I Q V H Y Y N D L L Q I A I A E S K *

44AHJDORF017

10757 atggaaagattaaaattgcttctgctggtataccgaaaaacgccttttgatacaagcgtcgattttgaaacctttgtacgtgaac
1 M E R L K L L L L V Y R K T P L I Q A S I L K P L Y V N
10673 aattctttgacggtgccattattgaaaacaataaaaagtatctataatgagcaaggtacaatatcgatatatccgtctaaaactg
SD-138950.1

29 N S L T V P L L K T I K V S I M S K V Q Y R Y I R L K L
10589 aaattgtatgtggtaatgtatatgatgaatattttactgatgaacttaatatga 10536
57 K L Y V V M Y M M N I L L M N L I *

44AHJDORF018

1098 atgttaattgggtactgtgtccataatcacgtattcttcactatattgtccaataaaatcttgctcttttagctaaccaattaaaa
1 M L I G T V S I I T Y S S L Y C P I K S C S L A N Q L K
1014 cgattacctaataatcgattaataaagtcctcattaatcttagggaataaatatttattacaaatgtttcgaacattgta
29 R L P N A I S I N K V S L I L G N K Y L F T N V S N I V
930 tttgaattatcccatgtgcgcaaatgtccaagattttgaataa 886
57 F E L S H L S P N V Q D F E *

44AHJDORF019

9836 atgttacctgggtttgtataagattcttttttgaataaagggtacaccaattgcttttttatatttttctggtaactgtgcatat
1 M L P G L Y K Y S F L N K G T P I A F L Y F S G N C A Y
9752 gtccagttaccaccaatcacacgaccacttttttcatttgggtgactgatttaccactaattggtttatgggtcgcgtcatca
29 V Q L P P I T R P L F P F G L T D L P L I G L W S P S S
9668 tcagtaggattagaactactactcccactatctacttga 9630
57 S V G L E L L L P L S T *

44AHJDORF121

16362 atggaaaatgaaacaaaaaacattgagttgaagcatgtttttcggttttaagaatggaagtttatgtatagcggtattttgataga
1 M E N E T K N I E L K H V F R F K N G S L C I A L F D R
16278 acagaaaatgaaattttcatttttatgatgttgacattgaaattgaagatttaaatcataaattctgttttacgcgtaatttca
29 T E N E I S F Y D V D I D E I E D L N H N S V L R V I S
16194 actttattaggaagtgtataaatgtgttaa 16165
57 T L L G S D N N G *

44AHJDORF020

13865 atgtctaaacgattttgtttttaccatgtttttgctccttgtaatatgtttatgatgtcgtttacagtgttaaattttattcgtaa
1 M S K R F C F T M F L L L V I V Y D V V Y S V K F I R Q
13949 atgttgataataataaaagtataacctcacatcttcatcatcaatatattgtcactggtctatctgatttaccattttctttat
29 M L H N I K S Y T S H L H H Q Y L S L V Y L I Y Q F L Y
14033 ataaagtatcgattttcttttaa 14053
57 I K Y R F L *

44AHJDORF123

614 atgtatgagggaacaacatgcggttctatgatgggtacatcatatgaagattcaagattaataaacgaacagaattaataatgaa
1 M Y E G N N M R S M M G T S Y E D S R L N K R T E L N E
698 aacatgtcaattgatacaaaatggaagtgaagatgtttgtgtacaaaattcattcactttcaaaacaatcatttacaggtgac
29 N M S I D T N K S E D S Y G V Q I H S L S K Q S F T G D
782 gttgaggaggaataa 796
57 V E E E *

44AHJDORF021

5816 atgcaccatcaaaagtcaacacctgccccctcatgcttatatatccattcttttgcttgttgttgatttcattttataatcactc
1 M H H Q S Q H L P P H A Y I S I L L V V V I S F I S L
5732 ctatttttgatgttttgcctaccacacatattcacgatgttttgtttccgcatttaacattactgaagaattctttatattccga
29 L F L M F C Y P T I F T M F C F R I N I T E E F F I F R
5648 tatattagcctctaa 5634
57 Y I S L *

44AHJDORF022

8611 atgtttgctaaaaatgataatacagaatatcaataatttttttagaaaatcctctcattgatttttttgaccataagttattattt
1 M F A K M I I Q N I N N F L E N P L I D F F D H K L L F
8527 ttaattgcttttgaataacctgtataatatcaacgaacattaatacaataaaaaagtag 8468
29 L I A F E I P V I I S T N I N T N K K *

44AHJDORF023

6494 atgagaacaccccccaaggaataaccaacactgtaaactattacctgtttttccattccattggcgactggtaataataacgtg
1 M R T P P K E Y Q H C N Y Y L F F H S I G A L V N N N V
6410 tgccttgccagttataaccaatccatacgtaacatctgtataacaaaacttcggttatatgggtgtataaccggttttggttgaacc
29 C L A S Y N Q S I R N H L I N K L R Y M V Y N R L V G T
6326 aatagccattag 6315
57 N S H *

44AHJDORF024

14275 gtgtcaatgtacgcctcttgttaaattctttatcatcaatttttaaaattaacattactaaaatcattttaaaaataaatctttttct
1 V S M Y A S C K S L S S N L K L T L L K S F K N K S F S
14359 tgctcttttctagcttctctttcttttttccatctatccatttcagacgtatgtctaaccaatgttatcaacctccatataaag
29 C S F L A S L S F F H L S I S D V C L T N V I N L H I K
14443 cataaataa 14451
SD-138950.1

57 H K *

44AHJDORF025

15175 atggaacgtaaatacaaaacgggtattattatattgcatgagattaaggacattttccacatcaaattctcaatgtttgaagat
 1 M E R K Y K T V L L Y C D E I K G H F P H Q I S M F E D
 15091 ttatatgacgctaaggtgtatattcatattatgaatataaacctgttcactaaaaataacgcgtatatcatagaatacattaag
 29 L Y D A K V V Y S Y Y E Y N L F T K K Y A Y I I E Y I K
 15007 gagatataa 14999
 57 E I *

44AHJDORF026

14593 atgaataacctattaaacatagccattgttttccttttagcatttttaattacacttatcatacttatgacactgcataacgc
 1 M N N L L N I A I V F L L A F L I T L I I L M T L H I R
 14509 gtgtcatttgggtgttttattcactacattgattatattctatattatctttttaatgggtattttatgcttttataggaggtga 14426
 29 V S F G V L F T T L I I F Y I I F L M V I Y A L Y G G *

44AHJDORF027

12916 atgattgtctatatccctaatttttagtataaaattcatattgttttgtatatggtacaacgataatatttgtcataaaagtagt
 1 M I V Y I P N F S T K F I L F C I W Y N D N I C H K S S
 13000 tacattatacatgactttaatatatttcatcagttttgatatagaagaatcacggttttgattgatgtgatttcttaa 13080
 29 Y I I H D F N I F I I S F D I E E I T V L I D V I S *

44AHJDORF029

15183 gtgttttaaatggaacgtaaatacaaaacgggtattattatattgcatgagattaaggacattttccacatcaaattctcaatgt
 1 V F K W N V N T K R Y Y Y I A M R L K D I F H I K S Q C
 15099 ttgaagatttatatgacgctaaggtgtatattcatattatgaatataaacctgttcactaaaaataacgcgtatatcatag 15019
 29 L K I Y M T L K L Y I H I M N I T C S L K N T R I S *

44AHJDORF028

9235 atggaatatatgcacgtccaattgtacctgctttcatatttttgcaaaatctgcattaccttttcttgtacgtcttggta
 1 M E Y M H V Q L Y L L S Y F L Q N L H Y L F F V R L V V
 9151 caaagtggacgatgttacctgcgtcataccaagacgggtgtccagctgttttgattgtgataactaactttcttctgatga 9071
 29 Q S G R C Y L R H T K T V V Q L V L I V I L T F L L *

44AHJDORF030

14487 gtgaataaaacaccaaataacacgcgtatatgcagtgatcataagtgataagtgtaattaaaaatgctaaaaggaaaacaatg
 1 V N K T P N D T R I C S V I S M I S V I K N A K R K T M
 14571 gctatgtttaataggttattcatggtcaatcactttccattatcgatatgactttgttttgataaataatcattaa 14648
 29 A M F N R L F M V N H F P I I V Y D F V L I N N H *

44AHJDORF031

11039 atgatatgtatagttcattgtttatcatctaaacggaataagttaaaatgtgaacgtaatgcaggtatgccatataatccattt
 1 M I L Y S S L L S S K R N K L K C E R N A G M P Y N P F
 11123 aaaacgacttttagataaacataacctcctcatttgagtagtgggtgttcgttgatatcatcagtaagtga 11191
 29 K T T L D N I T S S F E Y G C S L I S S V M *

44AHJDORF135

693 atgaaaacatgtcaattgatacaataaaaagtgagatagttatgggtgtacaaattcattcactttcaaaacaatcatttacag
 1 M K T C Q L I Q I K V K I V M V Y K F I H F Q N N H L Q
 777 gtgacgttgaggaggaataataaattatggcacaacaatctacaaaaatgaaactgcacttttag 842
 29 V T L R R N N K L W H N N L Q K M K L H F *

44AHJDORF033

3795 atgccattatttaaccacctctaccaaatttgtaaaaaacattttttatcaaattcatttaaaattttcttcttaaatcgtag
 1 M P L F N H L Y Q I C K K H F L S N S F K I F F L K S Y
 3711 gctttatcaatattatcaattaaatactgcttagtgaattgtgtaccttttgattacctttttga 3646
 29 A L S I L S I K Y C L V N C V P F A L P F *

44AHJDORF032

9455 atggcttgttttgctaaagcgagtagtgaactaccactgtcaccactactaccactgtcagacgaatcactaggtgatccaccc
 1 M A C F A K A S S E L P L S P L L P L S D E S L G D P P
 9371 ttaccgtctaatttaccaccccaagctagaatagtattcgcaccgtctaaaaatggattaccatag 9306
 29 L P S N L P P Q A R I V F A P S K N G L P *

44AHJDORF034

14146 atgatgattctaataataaaaaacgctaaaaagcataaatacgcttttatataatttacaagctaaaaataataattcttcaatgt
 1 M M I L I I K T L K S I N T L Y I I Y K L K I I I L Q C
 14062 ataaatatattaaagaaatcgatacttttatataaagaattggtaaatcagatagaccagtga 14000
 29 I N I L K K S I L Y I K K L V N Q I D Q *

44AHJDORF035

13957 atgcaacatttgacgaataaatttaacactgtaaacgacatcataaactattacaaggagcaaaaacatggtaaaacaaaatcg
 1 M Q H L T N K F N T V N D I I N Y Y K E Q K H G K T K S
 13873 tttagacatggtaagagattatcaaaatgctgtcattcatgtcagaaaaaaatcccagataa 13811
 29 F R H G K R L S K C C Q S C Q K K N P R *

44AHJDORF036

10165 gtgtatacaataaccacacgtgatgggtgcaacatatgggtgtacattatagtttgcaactaaaaacgaaccatcttcaaaaactg
 1 V Y T I P H V M V Q H M V V H Y S L Q L K T N H L Q K L
 10081 ctacaacaacacctgtgtgaccaataccatatgcagttgcttgtaagtatgggtggtttactag 10019
 29 L Q Q H L C D Q Y H M Q L L V S M V V Y *

44AHJDORF037

14788 atgtcgatatctaacgtaataaactctttttcaatttcaaaatcatcatattgtttgtcaactcaatatacacatcacccata
 1 M S I S N V N N S F S I S K S S Y C L S N S I Y T S P I
 14872 tttatttttactatacattttttattagatgaagtaaatttttcaatttatcattataa 14931
 29 F I F T I H F L L D E V N F S N L S L *

44AHJDORF038

3671 gtgtaccttttgcattacctttttgattttgattacgttttgcgttttgattactttcgttactcgattttattcacagttttac
 1 V Y L L H Y L F D F D Y V L R F D Y F R Y S I Y S Q F Y
 3587 cgttatcaatcgattattatcagcgaatcgtaacgtttgtattatcaacatcaatgttaa 3528
 29 R Y Q S Y Y Y Q R I V T L Y Y Q H Q C *

44AHJDORF039

1743 gtgctgtattttactttatgatgtatctaaacttaaagagtttactggcaacgttgaagaaattaaacaaaatcagattttatag
 1 V L Y L L M M Y L N L K S L L A T L K K L N Q N Q I Y M
 1827 cgtttttttggatattaattcaattaaatataaaacgttacacaaaaggatgttaa 1883
 29 R L F W I L I Q L N I N V T Q K V C *

44AHJDORF040

9740 gtggtaactggacatatgcacagttaccagaaaaatataaaaaagcaattgggtgtacctttattcaaaaaagaatacttatataca
 1 V V T G H M H S Y Q K N I K K Q L V Y L Y S K K N T Y T
 9824 aaccaggttaacatatttccctcaaacgggtaatgcaggacaatgtacagaattaa 9877
 29 N Q V T Y F L K R V M Q D N V Q N *

44AHJDORF041

15836 atgtcgtcaactttcattattatatactccttttctaaaaaacgtaaacgtttatcgtttcataaaatcctttatgcatattcc
 1 M S S T F I I I S L L S K K R K R Y T F H K I L Y A Y S
 15920 attgttctattgggtcatcaccagcaatataagacaattattgattctggttttag 15973
 29 I V L L G H H Q Q Y K T I L I L V *

44AHJDORF042

5151 atgcacgacgctgctcttttggtaatttatagttttgtgaacctcttgcgcgtaaatgcttcaaagtgttcatactcaccaagtt
 1 M H D R R L L L I Y S F V N L L R V M L Q S V H T H Q V
 5067 ggaagaaacctataaattatggaacggtttccaccacgcgctttgtcatag 5014
 29 G R N H I N Y G N V F H H R R L S *

44AHJDORF043

4539 atgcgacttgtaacagttttgcaacaccatcgatgtgaaccagattttcatttcaccattggattgacgtttcctaattccgattg
 1 M R L V T V L Q H H R D V T R F S F H H W I D V L I R L
 4455 ttgtaccatgaccacctgtacaatacgcgttgaaattatgattcaccactag 4402
 29 L Y H D H P V Q Y A C L K L S H H *

44AHJDORF044

12917 atgttacctattttacgtgatgatgttttataaagaaaacatggaacggttattactacaatccaagcaatttacattttgaca
 1 M L P I Y V M I C F I K K T W N V I T T I Q A I Y I L T
 12833 atgcttactctaaaaattacgtggttgataatgatagatatttatatttag 12783
 29 M L T L K I T W L I M I D I Y I *

44AHJDORF149

770 atgattgttttgaaagtgaatgaattgtacaccataactatcttcacttttattgttatcaattgacatgttttcatttaatt
 1 M I V L K V N E F V H H N Y L H F Y L Y Q L T C F H L I
 686 ctggtcgtttatttattccttgaaatcttcatatgatgtaccatcatag 639
 29 L F V Y L I L N L H M M Y P S *

44AHJDORF046

4891 atgattatccattttaagttatcatatcaagacggtattaatttcccacgtgataactttaagagcctgagggattttgcattt
 1 M I I H L S Y H I K T V L I S H V I T L K S L R V F A F
 4975 atacaaatccaaaaacaaaacgtaaatcgttattacttgctatga 5019
 29 I Q I Q K Q N V N R Y Y L L *

[illegible]

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44AHJDORF058

10767 atgcataattcttatgattcagtacaaacatcttatctatctgttcgttttcaatatcccatcttaaggtatcggtcga
1 M H I S Y D S V Q T S Y L S V R F Q Y P I Y L R L S G R
10851 ataaactggggttcaataagggttaa 10877
29 I N W G S I R V *

44AHJDORF164

702 atgttttcatttaattctgttcgtttatttaattcttgatcttcataatgatgtacccatcatagaacgcagtggtgtttccctca
1 M F S F N S V R L F N L E S S Y D V P I I E R M L F P S
618 tacatgtttaaattcctcctaattctaa 592
29 Y M F K F L L I *

44AHJDORF059

8360 atggattttgttaacattggattacctgaaccgctcattatgccaaaatcttacaccagattctaaaattgcttttaattgttcca
1 M D F V T L D Y L N R H Y A K I L H Q I L K L L L I V P
8276 ttaacatggggtcgatgtcacgtatag 8250
29 L T W G R C H V *

44AHJDORF060

6257 atgtaccattttcatttctataatatgtgccgtattgggttcgtttccattttccaaatgtatttacttttgatgtttctaag
1 M Y H F H F Y N M C R I G F V S I F Q M Y L L L M F L M
6173 ctttgctattactacctgaaaatttag 6147
29 L C Y Y Y L K I *

44AHJDORF061

15551 atgtgttttggtgtcttgataaaatatcttttacgtttgtcattttatttctcctcttattttaaattatttgctttctgcaatt
1 M C F G V L I K Y L L R L S F Y F S S Y L N Y L L S A I
15635 gcgattttagtaaatcattgtaa 15658
29 A I C S K S L *

44AHJDORF062

4285 gtggatttcgcaacgcagttaaccaatctattaatattgataaagaacaaatcacatgtactctacacaatccgatttctcaaa
1 V V F A T Q L T N L L I L I K K Q I T C T L H N P I L K
4369 aacctgaagggtttttggataa 4389
29 N L K V F G *

44AHJDORF063

9487 atgcgtcttgatttttttaataattcttgcatgggttgttttgctaaagcgagtagtgaactaccactgtcaccactactac
1 M R L V F F L I I L A W L V L L K R V V N Y H C H H Y Y
9403 cactgtcagacgaatcactag 9383
29 H C Q T N H *

44AHJDORF065

5029 gtgggtgaaaacgtttccataatttatatgggtttcttccaacttggtgagtatgaacactttgaagcattacgcgcaagaggtt
1 V V E N V S I I Y M V S S N L V S M N T L K H Y A Q E V
5113 cacaaaactataaattaa 5130
29 H K T I N *

44AHJDORF064

2609 atgacgagtcaatcaatcaacttggtgtccgaaatatataacggtgcaccatttgttaaaatgtcacctatgtttaatgcagatg
1 M T S Q S I N L C P K Y I T V H H L L K C H L C L M Q M
2693 acgatatcattgatttaa 2710
29 T I S L I *

44AHJDORF066

10481 atgatattctttatattgaaagtgcacatcggttcattttcacttaacgacttatttccagttgaacgttcagtacataacaaat
1 M I F F I L K V T S V H F H L T T Y F Q L N V Q Y I T N
10397 ctgatttgcataatattaa 10380
29 L I C I Y *